US-03-137-117B-28.rge

(ML)

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn Mon Jul 8 08:48:09 1996; MasPar time 264.75 Seconds 1018.838 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-137-117B-28 Title:

(1-381) from USO8137117B.seq 381 Description: Perfect Score:

1 ATGGTGTCCTCAGCTCAGTT.......GGACCAAGCTGGAAATAAAT 381
TACCACAGGAGTCGAGTCAA.......CCTGGTTCGACCTTTATTTA N.A. Sequence:

TABLE default

Gap 6 Scoring table:

Dbase 0; Query 0 Nmatch STD 264399 seqs, 353985056 bases x 2 Searched:

Listing first 45 summaries * Minimum Match Post-processing:

embl-new11 Database:

1:ECT 2:FUN 3:INV1 4:INV2 5:INV3 6:MAM 7:ORG 8:PLN 9:PR1 10:PR12 11:PR13 12:PR01 13:PR02 14:R0D 15:SYN 16:UNC 17:VRT 18:VIR

genbank 91

Database:

19:BCT1 20:BCT2 21:BCT3 22:BCT4 23:BCT5 24:BCT6 25:BCT7 26:INV1 27:INV2 28:INV3 29:INV4 30:INV5 31:MAM1 32:MAM2 33:PAT1 34:PATZ 35:PAT3 35:PAT3 35:PAT3 35:PAT4 30:INV5 31:MAM1 32:MAM2 40:PLM4 41:PLM5 42:PLM6 43:PLM7 44:PR11 45:PR12 46:PR13 47:PR14 48:PR15 49:PR16 50:PR17 51:PR18 52:PR19 53:ROD1 54:ROD2 55:ROD3 56:ROD4 57:ROD5 58:ROD6 59:ROD7 60:STR 61:SYN 62:UNA 63:VRL1 64:VRL2 65:VRL3 66:VRL4 67:VRL5 68:RUB6 69:VRL1 70:VRT2 71:VRT3

Database:

72:BCT1 73:BCT2 74:INV1 75:INV2 76:MAM 77:PHG 78:PLN 79:PR11 80:PR12 81:PR13 82:ROD 83:STR 84:SYN 85:UNA

86:VRL 87:VRT u-emb144_91

Database:

88:part1

Mean 10.298; Variance 3.799; scale 2.711 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

Pred. No.	0.00e+00					•	.00e+0	.00e+0	.00e+0	.00e+0		0.00e+00	.00e+0		0.00e+00		00e+	4.71e-300	-89g	.68e-	1.68e - 295	-989·	. 68e-	-88e-	-899	3.18e - 293	4.37e-292	.00e-	.00e-	.00e-	-900·	-900·	.00e-	.00e-2	.00e-2	.00e-2	.00e-2	.00e-2	-900·	.00e-2	-900·	<u>ş</u>	.23e-29	3e-28	1.13e-288
Description	Ig VL-anti-CD4 mAb M-	s musculus germli		7	Ig		ulus (clone	Ig kappa-c	Ig active	Ig kappa chain	earranged	gene for	gene for	is gene for	Mouse Ig rearranged k			M.musculus/ H.sapiens		gene for	M.musculus gene for i	rearranged			pabu	sculus Iq Fab	M.musculus NL4H10 mRN	Mouse Ig kappa germli	rearra	Ω	Mouse Ig kappa-chain		Ιđ	Ig kappa-	Ig kappa activ	M.musculus gene for i	Mouse Ig kappa-chain	Mouse Ig active kappa	Ig kappa-c	Mouse Ig active kappa	Ig active	kappa-c	Mouse Ig kappa-chain	ight-c	M.musculus gene for I
ΩI	550261	USI	MUSIGKAAAL	MM1 6689	MMU16689	MMU05217	MUSIGK527A	MUS I GKCKO	MUS I GKCPW	MUS I GKAAAM	MUS I GKAVD	MMIGKL229	MMIGKL38	MMI GKL233	MUS I GKAVE	MUSIGKAVE	S63022	MMHS2H1VL	MMIGLC151	MMIGKL4B0	MMIGKL4C1	MUSIGKAVA	MUSIGKAVH	MMIGKL218	MUSIGKAVJ	MMU20820	MMNL4H10	MUSIGKWJ	MUSIGKADT	MMIGVK36	MUSICKABT	MUS I GKCOD	MUSIGKAVC	MUSIGKCRS	MUSICKAAO	MMIGKL228	MUSIGKCRR	MUSICKCOB	MUSIGKCRP	MUS1GKCOC	MUSIGKCOA	MUSIGKCRT	MUSICKCRO	MUSICLAQ	MMI GHPS 6B
DB	59		26	14	82	54		26		26	26	54		54	26	99	59	53	54		54	99	99	54	26	54	54	99	99	54	99	99	99	26	26	54	26	26	26	26	26	96	26	96	53
Length	381	393	395	381	381	381	378	366	345	395	324	324	324	324	324	324	408	508	324	324	324	324	324	324	324	330	321	321	321	323	323	324	324	324	324	324	324	324	324	324	324	324	324	321	324
Query Match	92.9	92.9	92.4	91.9	91.9	90.3	90.0	88.2		82.9	81.4	81.4	81.4	81.4	81.4	81.4	80.8	79.3	78.2	78.2	78.2	78.2	78.2	78.2	78.2	77.7	77.4		•		•	•		•	77.2	•	•	•	•	•		76.9	Ġ.	16.6	
Score	354	354	352	350	320	344	343	336	328	316	310	310	310	310	310	310	308	302	298	298	298	298	298	298	298	596	295	294	294	294	294	294	294	294	294	294	294	294	294	294	294	293	293	292	292
Result No.	-	2	e	4	5	9	7	∞	6	10	11	12	13	14	15	16	11	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALI GNMENTS

S50261 381 bp mRNA ROD 02-APR-1993 Ig VL=anti-CD4 mAb M-T151 variable region light chain [32, chimeric antibody] [mice, hybridoma cells, mRNA Partial, 381 nt]. \$50261 DEFINITION ACCESSION RESULT LOCUS

mice hybridoma cells. ORGANISM KEYWORDS SOURCE

Mus sp. Unclassified.

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DEFINITION Mus musculus germline immunoglobulin light chain variable region and joining region mRNA, 5' end.	ACCESSION L35316 KEYWORDS germline; immunoglobulin light chain; joining region;	ORGANISM Mus musculus Enkaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;	Eutherla; Kodentla; Myomorpha; Murldae; Murnae. REFERENCE 1 (bases 1 to 393)		remyelination in a model of multiple scl	autoantibody encoded by germline immunoglobulin genes JOURNAL J. Immunol. 154 (5), 2460-2469 (1995)	E 3	COMMENT NCBI gi: 829182 FEATURES Location/Qualifiers	rce	/organism="Mus musculus" /strain="5JL/J"	/cell_line="SCH94.03"	/cell_type="hybridoma" /semienned_mol="mRNA"		<pre>sig_peptide 160 //ntc="putative" /function="leader peptide"</pre>	/codon_start=1 CDS 1>343		/codon start=1 /rroduct=":mm:noonlobulin light obsin"	/translation= //www.SAQFLGLLILCEQGTRCDIQMTQTTSSLSASLGDRVTISCR ASQDISNYIMYQERDGTVKLLIYTSRLASCPSRFSGSGSGTDYSLISNLEQED TAYYFCOOTAYTPWTFGGTKFLIKRADA"	mat peptide 61384	/note /codo	BASE COUNT 105 a 96 c 89 g 103 t ORIGIN	Query Match 92.9%; Score 354; DB 56; Length 393;	Similarity 96.6%; Pred. No. $0.00e+00;$ $67;$ Conservative $0;$ Mismatches $13;$	atgatqtectetqeteagtteettggteteetgttgetetgtttteaaggtaeeagatgt 60			61 GATATIC GAGATA A CAGACTA CATCACT CA	מו משועורימשמחומשימימשרומימורימימימימימימימימימימימימימימימימי	atcagttgcagggcaagtcaggacattagcaattatttaaactggtatcagcagaaacca 	Qy 121 ATCAGTTGCAGGCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA 180	gatggaactgttaaactcctgatctactacacatcaagattacactcaggagtcccatca	Qy 181 GATGGAACTATTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA 240	Db 241 aggttcagtggcagtgggtctggaacagattattctctcaccattagcaacctggagcaa 300
1 (bases 1 to 381) Weissenhorn, W., Scheuer, W., Kaluza, B., Schwirzke, M.	Flieger, D., Ienz, H., Weiss, E. H., Rieber, E. P., Riethmuller, G. et, al. Combinatorial functions of two chimeric antibodies directed to	Gene 121 (2), 2/1-2/8 (1992) 93077041	Genbank start at the National inbrary of Medicine created this entry (NCBI gibbsq 119499) from the original journal article.	This sequence comes from Fig. la. NCBI oi: 260761	6		"mice"	138] /partial		/note="Method: conceptual translation supplied by author. This sequence comes from Fig. 1a. NCBI gi: 260762"		/product="anti-CD4 mAb M-T151 variable region light chain" /franslation="MMSSADFLGILILEPOGREDIOWTOFTSSLGNBVT19GR	ASQDINAL SHYQQKPDGTK TOTAL TOT	VATIFCQQGNILPITFGGGIKLELK. IT 105 a 92 c 83 g 101 t	92.98	Similarity 96.6%; Pred. No. 0.00e+00; 67; Conservative 0; Mismatches 13; Indel	the state over the state of the state of the state of the state of the state over the state over the state of the state over t	augargiciciogociagociagociciogociciocogocicagogociagogocicagogociagogocicagogo	61 gatatecagatgacacagaetatatectecetettgeetettgggagacagagteace 120		l atcagttgcagggcaagtcaggacattaacaattatttaagctggtatcagcagaaacca 180			GATGGAACTATTAAACTCCTGATCTACACACATCAAGATTACACTCAGGAGTCCCATCA			משפתם ביותר בייתר		301 GAAGACATTGCCACTTACTTTTGCCAACAGGGTAACACGCTTCCGTACACGTTCGGAGGG 360	361 gggaccaagctggaaataaa 380 	· G	2	MUSIVJR 393 bp mrna rod 25-may-1995
REFERENCE AUTHORS	TITLE	MEDLINE	KEMAKK	COMMENT	FEATURES	sonice	ŧ	SCO						BASE COUNT ORIGIN	Onerv Match	Best Local Matches	£	3 &	qq	δ	Db 121	Ωy 1:	Db 181	Qy 181	Db 241	0v 2				Dp 3	Qy 361	RESULT	LOCUS

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ACCESS ION

KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS JOURNAL MEDLINE

TITLE

DEFINITION

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FEATURES COMMENT

mat peptide

J_segment

BASE COUNT ORIGIN

US-08-137-117B-28 rge Jul 8 08:42

ö gaagatattgccacttacttttgccaagagggtaacacgcttccttacacgttcggaggg 371 132 atcagttgcagggcaagtcaggacattagcaattatttaaactggtatcagcagaaacca 191 aggttcagtggcagtgggtctggaacagattattctctcatcattagcaacctggagcaa 311 12 atgatgtcctctgctcagttccttggtctcctgttgctctgtttcaaggtaccagatgt 71 Gaps White K.D., Frank M.B., Foundling S., Cummmings R.D., Waxman F.J.; "Effect of variable domain structure and CH2-linked carbohydrate on C3b and C4b deposition and classical complement pathway 03-NOV-1995 (Rel. 45, Created) 03-NOV-1995 (Rel. 45, Last updated, Version 1) Mus musculus Ig light chain leader and variable region Vk V gene ; 0 Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Submitted (27-OCT-1994) to the EMBL/GenBank/DDBJ databases. Length 395, 0; Mismatches 14; Indels Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae Score 352; DB 56; Pred. No. 0.00e+00;

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/translation="MMSSAQFLGLLLICFQGTRCDIQMTQTTSSLSASLGDRVTISCR ASQDISNYLAWYQQKPDGTVKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTISNLEQED Effect of variable domain structure and CH2-linked carbohydrate on C3b and C4b deposition and classical complement pathway activation Direct Submission Submitted (27-OCT-1994) Bart Frank, Arthritis and Immunology Program, Oklahoma Medical Research Foundation, 825 NE 13th Street, Oklahoma City, OK 73104, USA ö Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Mus. /cell_type="hybridoma (NS-1 x spleen cells) post DNP-BSA /note="encodes R1 through FR3 of immunoglobulin V-kappa" note="member of the murine Vk V gene family" /product="immunoglobulin light chain variable region" 346..381 gatatecagatgacacagactacatectecetgtetgeetetgggagacagagteace 120 121 atcagttgcagggcaagtcaggatattagcaattatttaaactggtatcagcagaaacca 180 240 9 9 Gaps gatggaactgttaaactcctgatctactacacatcaagattacactcaggagtcccatca and /codon_start=1 /product="immunoglobulin light chain precursor" .; 0 Length 381; White, K.D., Frank, M.B., Foundling, S., Cummmings, R.D. Indels 0; Mismatches 15; Score 350; DB 82; Pred. No. 0.00e+00; /note="Jkl encoded residues" 101 t IATYFCQQGNTLPWTFGGGTKLEIK" /organism="Mus musculus" /note="NCBI gi: 1041801" /note="leader region" 83 g Location/Qualifiers /clone="10/131C1F7" /strain="BALB/c" immunizations /sex="female Query Match 91.9%; Best Local Similarity 96.1%; 92 c (bases 1 to 381) 365; Conservative by immunoqlobulins 61..324 61..381 1041800 ...381 ...>38 1..60 Unpublished Waxman, F.J. ď NCBI gi: Frank, B. 105 misc feature sig_peptide Jegment V region source BASE COUNT Matches 61 181 TITLE JOURNAL AUTHORS AUTHORS REFERENCE REFERENCE JOURNAL CDS FEATURES TITLE COMMENT ORIGIN 셤 ð 셤 용 ð ð δ

181

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GGGACCAAGCTGGAAATAAA 380 ggcaccaagctggaaatcaa 380

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gaagatattgccacttacttttgccaacagggtaatacgcttccgtggacgttcggtgga

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240 181 gatggaattgttaaactcctgatctactacacatcaacattacactcaggagtcccatca q

δ 241 aggttcagtggcagtgggtctggaacagattattctctcaccattagcaacctggagcag 300 g

241 AGGITCAGIGGCAGIGGGICIGGAACAGAITAITCICICACCAITAACAACCIGGAGCAA 300 δ

g ð

361 ggcaccaagctggaaatcaa 380 임

361 ð

Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;

Eutheria; Rodentia; Myomorpha; Muridae; Mus.

(sites)

REFERENCE AUTHORS Suzuki, K.

Mus musculus

ORGANISM

005217 mouse.

ACCESSION

KEYWORDS

DEFINITION

MMU05217 381 bp mRNA ROD 20-MAY-1994 Mus musculus Balb/c anti-platelet integrin gpIIb/IIIa light chain immunoglobulin, partial cds.

A humanized antibody specific for the platelet integrin gpIIb/IIIa J. Immunol. 152, 2968-2976 (1994)

(bases 1 to 381)

94194058

JOURNAL MEDLINE Direct Submission

JOURNAL

Co, M.

REFERENCE AUTHORS

Co,M., Yano,S., Hsu,R.K., Landolfi,N.F., Vasquez,M., Cole,M.S., Tso,J.T., Bringman,T., Laird,W., Hudson,D., Kawamura,K. and

Submitted (14-JAN-1994) Man Sung Co, Protein Design Labs., Inc., 2375 Garcia Ave, Mountain View, CA 94043, USA

/organism="Mus musculus"

Location/Qualifiers

1..381 gi: 460600

source

FEATURES

COMMENT

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1..>381

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MUSIGK527A 378 bp mRNA ROD 25-JAN-1995 Mus musculus (clone 5-27) anti-fluorescein antibody (IgK) mRNA, DEFINITION

V-region. L39092 ACCESSION

V-region; V-segment; anti-fluorescein antibody; immunoglobulin kappa-chain; monoclonal antibody KEYWORDS

Mus musculus (strain BALB/c, sub_species domesticus) hybridoma cDNA SOURCE

Mus musculus ORGANISM

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

(sites) REFERENCE AUTHORS

Location/Qualifiers NCBI gi: 639666 90094387 JOURNAL MEDLINE FEATURES COMMENT

organism="Mus musculus" 1..378

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102

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83

92 c

104

mat_peptide BASE COUNT 1

90.3**%;** 95.3**%;**

362; Conservative

Matches

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Best Local Similarity

Query Match

/product="anti-platelet integrin gpIIb/IIIa light chain immunoglobulin"

SBS ö 1 atgatgtcctctgctcagttccttggtttcctgttgctctgttttcaaggtaccagatgt 60 Gaps ö Score 344; DB 54; Length 381; Pred. No. 0.00e+00; Indels 0; Mismatches 18;

61 gatatccagatgacacagactacatcctccctgtctgcctctctgggagacagagtcacc 120

1 ATGGTGTCCTCAGCTCCAGTTCCTTGGTCTCCTGTTTTCAAGGTACCAGATGT 60

301

301

to mRNA

Bedzyk, W.D., Herron, J.N., Edmundson, A.B. and Voss, E.W. Jr. Active site structure and antigen binding properties of idiotypically cross-reactive anti-fluorescein monoclonal antibodies J. Biol. Chem. 265 (1), 133-138 (1990) TITLE

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ATYFCQQGNTLPWTFGGGTKLEIN"

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/organism="Mus sig_peptide <142 /note="Ig kapp /codon start=	CDS <1.,>356 /note="Ig kapi 196896"	/codon start=: /translation=' NYMWXQKPDGT	mat_peptide 43366 /note="Ig kap /note="Ig kap /codon_start=	Chromosome 6	Best Local Similarity 96.4%; P Matches 349; Conservative Db 1 ttoettggteteetgttgetegt	9y 19 TICCTIGGICTCCTGTTGCTCTGT Db 61 actacatcctcctgtctgctct	b 121 caggacattacatatttaaca	Qy 139 CAGGACATAGCAGTAATTAAAC Db 181 ctgatccactacacatcaagatta		Ay 239 INTEGRACAGAITAILUINGCACU Db 301 ttttgccaacagggtaatacgctt	RESULT 9 LOCUS MUSIGKCPW 345 bp LOCUS DEFINITION Mouse Ig active kappa- ACCESSION M27193 KEYWORDS C-region; V-region; V- immunoglobulin-kappa; SOURCE Mouse spleen, cDNA to ORGANISM Mus musculus Eukaryota; Animalia; C Eutheria; Rodentia; My	REFERENCE 1 (bases 1 to 345) AUTHORS Kaartinen,M., Rocca-Se TITLE Combinatorial associat non-cross-reactive mon
<pre>mat_peptide 6153/8 /gene="Igk" /codo_start=1 /product="anti-fluorescein antibody"</pre>	BASE COUNT 103 a 93 c 82 g 100 t ORIGIN	Query Match 90.0%; Score 343; DB 56; Length 378; Best Local Similarity 95.5%; Pred. No. 0.00e+00; Matches 360; Conservative 0; Mismatches 17; Indels 0; Gaps 0;	Db 2 tgtcctctgctcagttccttggtctcctcttgctctgtttcaaggtaccagatgtgata 61	Db 62 tccagatgacacagactacatcctccctgtctgcctctctgggagacagagtcaccgtca 121	Db 122 gttgcagggcaagtcaggacattaacaattatttaaactggtatcagcagaaaccagatg 181 	Db 182 gaactgttaaactcctgatgtactacacatcaaaattacactcaggagtcccatcaaggt 241 	Db 242 tcagtggcagtgggtctggaacagattattctctcaccattagcaacctggagcaagaag 301 	<pre>Db 302 atattgccacttacttttgccaacagggtaatacgcttccgtggacgttcggtggaggca 361</pre>	Db 362 ccaagctggaaatcaat 378	∞	CHARANTE THUS MAINECALLY Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae. 1 (bases 1 to 366) AUTHORS Chen, MT., Kabat, E.A., Lundblad, A. and Ratcliffe, R.M. TILLE Nucleotide and translated amino acid sequences of cDNA coding for the variable regions of the light and heavy chains of mouse hybridoma antibodies to blood group A and B substances hybridoma antibodies to blood group A and B substances hybridoma antibodies to blood group A and B substances wEDLINE 88007582 COMMENT Draft entry and printed copy of sequence for [1] kindly provided by E.A. Kabat, 04-ANG-1987.	NCBI gi: 196895 FEATURES Location/Qualifiers

n="flgllllcroggtrodiomtottsslasigdrutiscrasodin stykllihttsrlhsgvpsrfsgsgsgstdysltisnleoediatyfc sctkleikr" Serra, J. and Maekelae, O. ation of V genes: One V-H gene codes for three onoclonal antibodies each specific for a <u>;</u> ppa-chain precursor V-region (VJ); NCBI gi: acactcaggagtcccatcaaggttcagtggcagtggg 240 ttctgggagacagaqtcaccatcagttgcagggcaagt 120 mRNA ROD 15-MAR-1990 a-chain mRNA V-J5 region, clone 18C10. Gaps Chordata; Vertebrata; Mammalia; Theria; Myomorpha; Muridae; Murinae. V-region; immunoglobulin light chain; 0; Score 336; DB 56; Length 366; Pred. No. 0.00e+00; 0; Mismatches 13; Indels uppa-chain signal peptide" :=1 ; processed gene. o mRNA, clone 18C10. ų 93 us musculus" appa-chain" t=1 81 g

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/translation="MMSSAQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCS A SQGI SNYLNWYQQKPDGTVKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTISNLEPED ö VH gene segments 61 GATATCCAGATGACACAGAGTACATCCTCCCTGTCTCTCCGGAGACACAGAGTCACC 120 251 132 atcagttgcagtgcaagtcagggcattagtaattatttaaactggtatcagcagaaacca 191 72 gatatccagatgacacagactacatcctccctgtctgcctctctgggagacagagtcacc 131 Gaps gatggaactgttaaactcctgatctattacacatcaagattacactcaggagtcccatca ; 0 Length 395; 0; Mismatches 32; Indels induced anti-Z-DNA monoclonal antibodies use related to those of anti-DNA autoantibodies Score 316; DB 56; Pred. No. 0.00e+00; /sequenced_mol="cDNA to mRNA" J. Immunol. 146 (6), 2005-2009 (1991) 91170743 IATYFCQQYSKFPFTFGSGTKLEIKR" 110 /cell_line="hybridoma Z22" /product="Ig kappa chain" /product="Ig kappa chain" /organism="Mus musculus" /note="NCBI gi: 196426" 357..35J /gene="lgM" /map="chromosome 6" ^A A 86 g /tissue_type="liver" •9 **5** /map="chromosome 6" Location/Qualifiers /dev_stage="fetus" /map="chromosome /gene="IgM" /map="chromosome /map="chromosome /codon_start=1 12..395 /codon_start=] /codon start= /gene="IqM" /gene="IgM" Query Match 82.9%; Best Local Similarity 91.6%; Matches 348; Conservative /gene="IgM" /partial 72..356 12.395 1..395 NCBI gi: 196425 105 a Chromosome 6. sig_peptide mat_peptide J_segment V_region source BASE COUNT 192 MEDLINE JOURNAL SGS FEATURES TITLE COMMENT ORIGIN 유 임 셤 õ 셤 8 셤 δ ò

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KEYWORDS

SOURCE

RESULT

TITLE

TITLE

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FEATURES

COMMENT

US-08-137-117B-28.rge Jul 8 08:42

translation qualifiers on V redion features are illegal." /translation="DIOMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTV KLLIYYTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLP" Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; ö Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Submitted (14-JAN-1991) to the EMBL/CenBank/DDBJ databases. L.J. Wysocki, NATIONAL JEWISH CENTER FOR IMMUNOLOCY AND RESPIRATORY MEDICINE, DEPT OF PEDIATRICS K902, 1400 JACKSON ST, DENVER CO 80206, USA GATGGAACTATTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA 240 241 AGGTCAGTGGCAGTGGGTCTGGAACAGATATTCTCTCACCATTAACAACCTGGAGCAA 300 300 gatggaactgttaaactcctgatctactacacatcaagattacactcaggagtcccatca 180 aggitcagiggcagigggictggaacagaitaitcicicaccaitagcaacciggagcaa 240 8 M.musculus gene for immunoglobulin kappa light chain variable translation of the corresponding V region. Presently Gaps Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; 1 gatatecagatgacacagaetacatectecetgtetgeetetetgggagacagagteace ö Length 324; Score 310; DB 56; Lengtn John Pred, No. 0.00e+00; Sciurognathi; Myomorpha; Muridae; Murinae; Mus. 16 immunoglobulin kappa light chain /note="VKIdCR segment" 285..>324 /note="JK2 segment" Б DNA 301 gggaccaagctggaaataaa 320 361 GGACCAAGCTGGAAATAAA 380 /gene="IgK" /map="6" ď /gene="IgK" Best Local Similarity 98.4%; 81.48; (bases 1 to 324) 78 c 315; Conservative 324 Direct Submission /map="6" region (KL2.29). <1..284 chromosome 6. Mus musculus Wysocki, L.J. house mouse.

to 324)

REFERENCE AUTHORS

TITLE

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Jul 8 08:42

vitro

JOURNAL AUTHORS REFERENCE

TITLE

source

CDS

COMMENT FEATURES

JOURNAL MEDLINE

US-08-137-117B-28.rge

(KL3.8)

86

BASE COUNT

ORIGIN

Query Match

Matches

유 ð q 121

Q ð 셤 ð 셤 ð

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241 241 301 301

181

misc_feature

MMIGKL38

DEFINITION

13

RESULT

LOCUS

361

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Wysocki, L.J., Creadon, G., Lehmann, K.R. and Cambier, J.C. B-cell proliferation initiated by Ia cross-linking and sustained by interleukins leads to class switching but not somatic mutation in /translation="DI@MTQTTSSLSAS.LGDRVTISCRASQDISNYLMMYQQRPDGTV KLLIYYTSRLHSGVPSRFSGSGGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGT ፩ Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; interleukins leads to class switching but not somatic mutation in ö Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Wysocki, L.J., Crendon, G., Jehmann, K.R. and Cambier, J.C. B-cell proliferation initiated by Ia cross-linking and sustained Direct Submission Submitted (14-JAN-1991) to the EMBL/GenBank/DDBJ databases. L.J. 61 GATATCCAGATGACACAGAGTACATCCTCCCTGTTGCCTCTCTGGGAGACAGAGTCACC 120 61 atcagttgcagggcaagtcaggacattagcaattatttaaactggtatcagcagaaacca 120 121 ATCAGTTGCAGGGCAAGTCAGGACATTAGCAGTTATTAAACTGGTATCAGCAGAAACCA 180 Wysocki, NATIONAL JEMISH CENTER FOR IMMUNOLOGY AND RESPIRATORY MEDICINE, DEPT OF PEDIATRICS K902, 1400 JACKSON ST, DEAVER CO 9 Gaps Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; 1 gatatecagatgacacagaetacatectecetgtetgeetetetgggagaeagagteaee ; 0 /product="immunoglobulin kappa light chain" Score 310; DB 54; Length 324; Pred. No. 0.00e+00; 0; Mismatches 5; Indels Sciurognathi; Myomorpha; Muridae; Murinae; Mus. /cell_type="B lymphocyte"
/cell_line="hybridoma; KL3.8" 76 t

Jul 8 08:42 US-08-137-117B-28 rge	Oriun Query Match 81.4%; Score 310; DB 54; Length 324; Best Local Similarity 98.4%; Pred. No. 0.00e+00; Matches 315; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	gatatccagatgacacagactacatcctccctgtctgcctcttgggagacagagtcacc 60	<pre>Db 61 atcagttgcaggcaagtcaggacattagcaattatttaaactggtatcagcagaaacca 120 </pre>	Db 121 gatggaactgttaaactcctgatctactacacatcaagattacactcaggagtcccatca 180 	Db 181 aggttcagtggcattggaacagattattctctcaccattagcaacttggagcaa 240	Db 241 gaagatattgccacttacttttgccaacaggtaatacgcttccgtacacgttcggaagg 300	361 GGGACCAAGCTGGAATAAA	RESULT 15 LOCUS MUSICKAVF 324 bp DNA ROD 29-OCT-1994 DEFINITION Mouse Ig rearranged kappa-chain (V-IdCR J2) gene V10-J region, hybridoma KI3 R. narfial cds.	ION	_	AUTHORS Sakano, H., Huppl, K., HelfillCfl, G. and lonegawa, J. TITLE Sequences at the somatic recombination sites of immunoglobulin light-chain genes JOURNAL Nature 280 (5720), 288-294 (1979)	79221879 2 (sites) Wysocki, L. J., Gridley, T., F	Get Sin var p-a J.	JUDKNAL IMMUDOLOGY /3 (1), 118-121 (1992) MEDLINE 92165291 COMMENT NCBI gi: 196788
Jul 8 08:42 US-08-137-117B-28.1ge 19	Db 181 aggttcagtggcagtgggtctggaacagattattctctcaccattagcaacctggagcaa 240 	241 gaagatattgecacttacttt 	Db 301 gggaccagctggaaataaa 320 	RESULT 14 LOCUS MMIGKL233 324 bp DNA ROD 05-NOV-1994 DEFINITION M.musculus gene for immunoglobulin kappa light chain variable region (KL2.33).	ACCESSION X55045 KEYWORDS immunoglobulin kappa light chain. OURGE nouse mouse.		REFERENCE I to 324) AUTHORS Mysocki, L.J. TITLE Direct Submission	1 [:	Mys B-c int	JOURNAL Unpublished NEFERENCE 3 (bases 1 to 324) AUTHORS Mysocki,L.J., Creadon,G., Lehmann,K.R. and Cambier,J.C. TITLE B-cell proliferation initiated by Ia cross-linking and sustained by	Interleuking leads to class Switching but not somatic mutation in vitro JOURNAL Immunology 75 (1), 116-121 (1992) WEDLINE 92165991	NCBI gi:	/organism="Mus musculus" /cell_type="B lymphocyte" /cell_line="hybridoma; KL2.33" /chromosome=="6" <l524 <="" note="NCBI gi: 511032" td=""><td>misc_reature 285324 /note="Jk2 segment" BASE COUNT 98 a 78 c 72 g 76 t</td></l524>	misc_reature 285324 /note="Jk2 segment" BASE COUNT 98 a 78 c 72 g 76 t

Socation/Qualifiers

source

FEATURES

/organism="Mus musculus" /strain="(CAL-20 x A/J) F1" /cell_line="hybridoma KL3.8"

/tissue_type="B lymphocyte"

'gene="IgK"

SBS

/map="6"

/sequenced_mol="DNA"

translation of the corresponding V_region. Presently translation qualifiers on V_region_features are illegal." /translation="DIQMTQTTSSLSASLGDRVTISCRASQDISNYLWWYQQKPDGTV KLLIYYTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLP"

/note="This CDS feature is included to show the

/gene="IgK"

<1..>284 /map="6"

CDS

KLEIKR"

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Gaps

; 0

Length 324; Indels

Score 310; DB 56; Pred. No. 0.00e+00;

81.48;

Query Match Best Local Similarity

0; Mismatches

315; Conservative

Matches

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/note="JK2 segment" 78 c 72 g

chromosome 6.

98 a

BASE COUNT

ORIGIN

/gene="IgK" /map="6"

/note="VKIdCR segment" 285..>324

Jegment

/gene="IgK" /map="6"

<1..284

V_region

61 atcagttgcagggcaagtcaggacattagcaattatttaaactggtatcagcagaaacca 120

1 gatatecagatgacacagaetacatectecetgtetgeetetetgggagacagagteace 60

gatggaactgttaaactcctgatctactacacatcaagattacactcaggagtcccatca 180 aggttcagtggcagtgggtctggaacagattattctctcaccattagcaacctggagcaa 240

121

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gaagatattgccacttacttttgccaacagggtaatacgcttccgtacacgttcggaggg 300

241 301

q õ අ δ

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gggaccaagctggaaataaa 320

361

301

/product="immunoglobulin kappa chain" /translation="DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQKRDGTV KLLIYYTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGT

associated with strain A response to p-azophenylarsonate; NCBI gi: 196789*

/codon_start=1

/note="light chain variable region of antibodies

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Search completed: Mon Jul 8 08:52:40 1996 Job time : 271 secs.

US-08-137-117B-28 mg

Jul 8 08:43

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn Mon Jul 8 08:52:57 1996; MasPar time 33.66 Seconds 752.688 Million cell updates/sec Run on:

Tabular output not generated.

Title:

>US-08-137-117B-28 (1-381) from USO8137117B.seq 381

1 ATGGTGTCCTCAGCTCAGTT.......GGACCAAGCTGGAAATAAAT 381
TACCACAGGAGTCGAGTCAA........CCTGGTTCGACCTTTATTA Description:
Perfect Score:
N.A. Sequence:
Comp:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 Nmatch STD 84802 seqs, 33246950 bases x 2 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

n-geneseq22 1:partl 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16

Mean 8.229; Variance 4.974; scale 1.655 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Regult No.	Sco	Query Match	Query re Match Length DB I	DB	A	Description	Pred. No.
1	381	100.0	381	5 0	030755	pPM-k3.	2.64e-243
2	354	92.9	38]	9	036607	Anti-CD4 antibody MT	2.63e-224
٣	354	95.9				MAb SCH94.03 light ch	2.63e-224
4	344	90.3		7		Mouse C4G1 Iq light-c	2.82e-217
S	340	89.5		S	809800	ME4 Light Chain V Reg	1.82e-214
9	334	87.7		2	030759	p146-k3.	2.98e-210
7	323	84.8				Human IL-1 chimeric a	1.57e-202
œ	322	84.5	402	7	012017	Sequence encoding mou 7	7.88e-202
9	322	84.5				Sequence encoding lig	7.88e-202

<u> </u>	30e-	11	6.41e-169	14	2.66e-122	6.44e-121	2.19e-115	5.28e-114	3.05e-111		3.05e-111	3.58e-109	1.75e~108		1.00e-105	2.77e-102	1.35e-101	6.59e - 101	_	_	3.21e-100	3.21e-100	7.61e-99	3.70e-98	3.70e-98	3,70e-98	1.80e - 97	1.80e - 97	1.80e - 97	1.80e - 97	1.80e - 97	8.75e-97	6	4.25e-96
dolpounum	KM641 H Chain Variabi R-cell lymphoma CH12	Bispecific CD3-L6FvIg	Anti-influenza N10 sc	Monoclonal antibody 1	Humanized 1308F VL DN	Sequence encoding the	H65 light chain varia	Plasmid pXOM2.	Light chain variable	Light chain variable	Light chain variable	ice encoding		equence encoding 520		equence encoding G-F	3KA9 anti-Varicella	region gene JP2gL41	eline immunoglobulin	Sequence encoding the	equence of the VL re	KM-603 light chain.	Human anti-HBs light	Murine OKT4A light ch	ME1-14 light chain va	V-J(gamma)/[(Gly)4Ser	Humanised antibody he	Encodes kappa chain V	ci-IL2R-alpha antib	-2 chimeric antibod	chimeric a	cDNA contg. an ORF fo	Encodes light chain o	V-J (kappa) / [(Gly) 4Ser
)58 138	x ; a	976	957	294	194	-		Q34574 Pla					_			S	9	>	Q10946 Fe.	-		_	Q49943 Hw	012631	073537	042285	075546	042268	036611		015114	067895	020067	042284
408 6	324 16	-	-	, -i	389 14	-	400 1	388	_	-	321 16	419 1	H	739 8	Н	1605 8	387 14	618 2	618 2	702 7	384 11	Ţ			-		Н	321 7	_	432 3		7	945 3	723 7
79.8	9.8						52.0	51.4	50.4	50.4				49.1							•	46.2	'n	•	45.4	ŝ	45.1	•	•		5	44.9	4	4.
304	304 294	280	275	244	208	206	198	196	192	192	192	189	188	187	184	179	178	177	177	177	176	176	174	173	173	173	172	172	172	172	172	171	171	170
10	1 1	13	14	15	16	11	18	19	20	21	22	23	24	52	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	45	43	44	45

ALI GNMENTS

	Human, antibody; interleukin-6; receptor; II-6R; light chain; L; H; heavy chain; variable region; mouse; monoclonal; hybridoma; PM1; plaamid; pPM-h1; ss.		suchiya M;
A; 381 BP.	Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; heavy chain; variable region; mouse; monoclonal; hybridoma; PMI; plasmid; pPM-k3; pPM-h1; ss.	Location/Qualifiers 160 61381	M09219759-A. 12-N0V-1992. 24-ART-1992. JU0544. 25-ART-1991; JP-095476. 19-FEB-1992; JD-032084. (CHUS) CHUGAL SEIYAKU KK. Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M; WRI; 92-398882/48.
RESULT 1 1D 030755 standard; CDNA; 381 BP. AC 030755; DT 30-MAR-1993 (first entry) DE PPM-K3.	Human; antibody; interleukin- heavy chain; variable region plasmid; pPM-k3; pPM-h1; ss.	Synthetic. Key Sig peptide 160 /*tag= a mat_peptide 61381 /*tag= b	W09219759-A. 12-NOV-1992. 24-ARR-1992; J00544. 25-ARR-1991; JP-095476. 19-FEB-1992; JP-032084. (CHUS) CHUGAI SEIYAKU KK. Bendig MM, Jones ST, Salda WPI; 92-38882448.
RESU ID AC DT DE	\$ \$2 \$2 \$2	SELLEE	PN PP PR PA DR

P-PSDB; R28670. Reconstituted human antibody to human interleukin-6 receptor

DR PT

Query Match

Matches

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US-08-137-117B-28 mg Jul 8 08:43

Monoclonal antibody; MAb; SCH94.03; hybridoma; central nervous system; CNS; demyelination; multiple sclerosis; neural disease; therapeutic; 300 360 gatatocagatgacacagactatatoctocotctctgoctctctgggagacagagtcaco 120 61 GATATCCAGATGACACGACTACATCCTCCTGTCTGCCTCTGGGAGACAGAGTCACC 120 121 atcagttgcagggcaagtcaggacattaacaattatttaagctggtatcagcagaaacca 180 GAAGACATTGCCACTTACTTTTGCCAACAGGGTAACACGCTTCCGTACACGTTCGGAGGG 360 anti-CD4 monoclonal antibody for use in the claimed synergistic composition. MAb WT 15.1 is deposited as clone 15-1/P3/14 (ECACC 90090705). The anti-CD4 antibody is used with at least one anti-IL2R alpha or beta antibody. Individually the antibodies are strongly 8 9 This sequence encodes the light chain variable region of a preferred inhibiting and when used together their immunosuppressive properties Gaps 241 AGGTTCAGTGGCAGTGGGCTCTGGAACAGATTATTCTCTCACCATTAACAACATGGAGGAA aggttcagtggcagtgggtctggaacagattattctctcaccattaccaacctggagcaa gaagatgttgccacttacttttgccaacagggtaatacgcttccgtacacgttcggaggg comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R proliferation to effectively inhibit transplant rejection at low doses without significantly reducing the general immune response ; Length 381; as immunosuppressant 101 T; 0; Mismatches 13; Indels are improved; they synergistically inhibit T-helper cell Query Match 92.9%; Score 354; DB 6; LA Best Local Similarity 96.6%; Pred. No. 2.63e-224; 83 G; Weidle Scheuer W, 92 C; compsn. for use or anti-IL2R beta antibodies Location/Qualifiers

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367; Conservative

Matches

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Best Local Similarity

Query Match

Sequence

Miller DJ, Rodriguez M; WPI; 95-393077/50. P-PSDB; R84553.

the CNS.

29-APR-1994; US-236520. (MAYO-) MAYO FOUNDATION 27-APR-1995; U05262.

W09530004-A1 mat_peptide

sig_peptide

Jul 8 08-43

/*tag= b

09-NOV-1995

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Gaps

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102 T;

chain.

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29-NOV-1993 (first entry)

RESULT
ID 04
AC 04
AC 04
DT 29
DE M0
KW IM

045662;

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US-08-137-117B-28 mg

JT 6 Q30759 standard; cDNA; 381 30-MAR-1993 (first entry) 030759; 181 241 241 Matches Best RESULT g 엄 g ð 셤 ð 염 à ò ð ð chimeric antibody mol. comprising two light chains and two heavy chains, each having a constant region (human) and a variable region (murine) ö 240 180 300 240 360 300 61 atgatgtcctctgctcagttccttggtctcctgttgctctgttttcaaggtaccagatgt 120 gatatecagatgacacagactacatecteeetgtetgeetetetgggagacagagteace 180 gaagattttgccacttacttttgccaacagggtaatatacttcctcggacgttcggtgga 420 GAAGACATTGCCACTTACTTTTGCCAACAGGGTAACACGCTTCCGTACACGTTCGGAGGG 360 9 having specificity to an antigen bound by murine monoclonal antibody (MAb) ME4. The chimeric antibodies can be used for any purpose for 0; Gaps which the original murine MAbs can be used, with the advantage that Claim 13; Page 123 + Fig 29; 173pp; English. Shown is the nucleotide sequence from the end of the oligo-dC tail to the Jkl-Ck junction. The sequence is used in the prodn. of a 1 AIGGECTCTCAGCTCAGTTCCTTGGTCTCTTTCTTCAAGGTACCAGATGT GATGGAACTATTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA aggttcagtggcagtgggtctggaacagattattctctcaccattagcaacctggagcaa gatggaactgttaaactcctgatctactacacatcaagattacactcaggagtcccatca for constant human region murine variable region, esp. to 3 tumour they are more compatible with the human body. They are esp. Monoclonal antibody; chimera; light; heavy; chain; constant; Chimeric mouse-human antibodies - prepd. using genes coding 89.2%; Score 340; DB 5; Length 444; 94.7%; Pred. No. 1.82e-214; 20; Indels Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP, variable; antigen; diagnosis; cancer; tumour; ss 94 G; 0; Mismatches 122 C; treatment of cancer. Location/Qualifiers Light Chain V Region (mouse) (ITGE-) INT GENETIC ENG INC. Conservative US-243739, US-253002, US-367641 US-240624 US-241744 US-382768 Best Local Similarity U03852 WPI; 90-115825/15. P-PSDB; R09426. the diagnosis and 08-SEP-1988; 13-SEP-1988; 19-JUN-1989; 21-JUL-1989; 360; 06-SEP-1989; 06-SEP-1988; 04-0CT-1988; Mus musculus /*tag= a WO9002569-A. 04-MAR-1993 22-MAR-1990 Sequence Query Match antigen 301 241 121 5 241 181 361 Matches අු 용 à 엄 a 음 염 δ

361 GGGACCAAGCTGGAAATAAA ggcaccaaactggaaatcaa 421 9

BP.

ö Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H; heavy chain; variable region; mouse; monoclonal; hybridoma; AUK146-15; The sequences given in Q30759 and Q31337 were used in example to illustrate the production of a human antibody which recognises human interleukin-6 receptor (IL-6R). The antibody comprises light (L) chain and heavy (H) chain variable regions which were derived from a mouse monoclonal antibody produced from the hybridoma AUK146-15 which sequence 381 Bp; 106 A; 90 C; 86 G; 99 T; Gaps has low antigenicity and contains mouse V-region complementarity . 0 Reconstituted human antibody to human interleukin-6 receptor / Match 87.7%; Score 334; DB 5; Length 381; Local Similarity 93.9%; Pred. No. 2.98e-210; 0; Mismatches 23; Indels (CHUS) CHUGAI SEIYAKU KK. Bendig MM, Jones ST, Saldanha JM, Sato K, Tsuchiya WPI; 92-398882/48. Disclosure; Page 127-128; 207pp; Japanese. Location/Qualifiers plasmid; p146k3; p146-h1; ss. 357; Conservative 25-APR-1991; JP-095476. 19-FEB-1992; JP-032084. 61..381 1..60 24-APR-1992; J00544. determining regions P-PSDB; R29010 sig peptide mat_peptide W09219759-A 12-NOV-1992 Synthetic. /*tag= b /*tag= a Query Match p146-k3.

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antibody or is a mouse-human graft containing the CDR regions of mouse anti-human IL-1 antibody, and a heavy (H) chain in which the constant recombinant antibody against human interleukin-1 (IL-1). The antibody has a light (1) chain in which the constant region is that of a human region is that of a human antibody and the variable region is from a mouse anti-human IL-1 antibody or is a mouse-human graft containing the CDR regions of mouse anti-human IL-1 antibody,. The chimeric antibody is used to treat diseases in which abnormal amounts of IL-1 are produced, eg. inflammatory disease, arteriosclerosis, diffused intravascular coagulation or leukemia. It can also be labelled and Probe; chimeric; recombinant; antibody; human; interleukin-1; II-1; light; L; chain; constant; region; variable; mouse; anti-human; The sequences given in 056066-69 are the coding sequences for the light and heavy chain, variable and constant regions of a chimeric abnormal, and for diagnostic imaging of interleukin-1 production antibody and the variable region is from a mouse anti-human IL-1 Mouse/human chimeric antibody against human interleukin-1 - for treatment of diseases in which production of interleukin-1 is used for diagnostic imaging of IL-1 producing sites in vivo. graft; CDR; complementarity determining region; heavy; H; inflammatory disease; arteriosclerosis; detection; 96 T; diffused intravascular coagulation; leukemia; ss. 78 G; Hirai Y, Nishida T, Omoto Y, Owens RJ; WPI; 94-048885/06. P-PSDB; R47206. 93 C; Q56067 standard; cDNA to mRNA; 372 BP 09-AUG-1994 (first entry) Human IL-1 chimeric antibody CH cDNA. Claim 1; Page 31-32; 58pp; Japanese. Location/Qualifiers 105 A; (SAKA) OTSUKA PHARM CO LTD. 94..372 08-JUL-1993; J00941. 16-JUL-1992; JP-189248. 372 BP; sites in vivo /*tag= b WO9402627-A. /*tag= a mat_peptide sig peptide 03-FEB-1994 Synthetic. Sequence A PART OF THE PART

Query Match
Best Local Similarity 93.5%; Pred. No. 1.57e-202;
Matches 347; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

- 61 atgacacagactacatcctcctgtctgcctctctgggagacagagtcaccatcacttgc 120

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Jul 8 08:43 US-08-137-117B-28 mg

ö 249 240 309 360 310 GCCACTTACTTTTGCCAACAGGGTAACACGCTTCCGTACACGTTCGGAGGGGGGACCAAG 369 82 gatatecagatgacacagactacatectecetgtetgeetetetggggagacagagteace 141 142 atcagttgcagtgcaagtcagggcattagcaattatttaaactggtatcagcagaaacca 201 241 ggcagtgggtctggaacagattattctctcaccattagcaacctggaagaagaagatgct 300 81 70 ATGACACAGACTACATCCTCCCTGTCTCCTCTCTGGGAGACAGAGTCACCATCAGTTGC 129 0; Gaps New chimeric mouse human antibodies - used in treatment, diagnosis ይ 150 GCGAGTGGGTCTGGAACACATTATTCTCTCACCATTAACAACTGGAGCAAGAAGAACATT 181 qttaaactcctqatctactacacatcaaqattacactcaqqaqtcccatcaaqqttcaqt gccacttacttttgccaacagggtaaaacccttccgtggacgttcggtggaggcaccaag 22 atgatgtcctctgctcagttccttggtctcctgttgctctgttttcaaggtaccagatgt human Abs against HIV-1 comprising human Ig constant regions and The mouse VL gene product may be used to produce chimeric mousetreatment, diagnosis and prophylaxis of HIV infections, and may produced by a bacterial, yeast or mammalian expression system. Sequence $402~\mathrm{BP}_i$ $108~\mathrm{A}_i$ $99~\mathrm{C}_i$ $88~\mathrm{G}_i$ $107~\mathrm{T}_i$ ^ Match
84.5%; Score 322; DB 2; Length 402;
Local Similarity 92.4%; Pred. No. 7.88e-202; Indels murine variable regions. These novel sequence are useful Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR; Sequence encoding mouse MAb 1C11 L chain V region. 0; Mismatches 29; Location/Qualifiers 22..402 Disclosure; Fig 13; 108pp; English. and prophylaxis of HIV infections. JT 8 Q12017 standard; DNA; 402 BP. 19-AUG-1991 (first entry) 351; Conservative 13-NOV-1989; US-433703. 370 CTGGAAATAAA 380 361 ctggaattcaa 371 HIV-1; chimera; ds. 13-NOV-1990; U06627 WPI; 91-178106/24. (XOMA-) Xoma Corp. P-PSDB; R12237. 30-MAY-1991. /*tag= a W09107494-A, Query Match 012017; Mus sp. Matches 61 301 Best g ð 음 g à දු 셤 Db ð 셤 δ g ò δ à õ

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	Db 82 gatatccagatgacacagactacatcctcctgtctgcctctctgggagacagagtcacc 141	Db 142 atcagttgcagtcagggcattagcaattatttaaActggtatcagcagaaacca 201	Db 202 gatggaactgttaaactcctgatctattacacatcaagtttacactcaggagtcccatca 261	Db 262 aggttcagtggcagtgggtctgggacagattattctctcaccatcagcaacctggaacct 321	Db 322 gaagatattgccacttactattgtcagcagtatagtaagcttccgtggacgttcggtgga 381	Db 382 ggcaccaagctggaaatcaa 401 	RESULT 10	ib y37036 standard; unk; 408 bk. AC 037058:	12-JUL-1993 (first entry) Rat immunoglobulin L chain varible region of pKM641LA2.	KW Promoter; variable; region; rat; immunoglobulin; heavy; H; chain; KW humanised; chimeric; antibody; expression vector; ss.	OS Rattus rattus. FH Key Location/Qualifiers			FT *tag= b FT mat_peptide 85408		PF 18-SEP-1992; 116026. PR 18-SEP-1991; JP-238375.	(KYOW) KYOWA HAKKO KOGYO CO LTD.	Hanal N, Hasegawa M, WPI; 93-095510/12.		PS Claim 6; Page 30-31; 63pp; English. CC The segmences given in 037057-58 encode rat heavy and light chain	CC variable regions respectively. These sequences were used in the	CONSTITUTION OF NUMBALISED CONTINUENCE AND ACTOR STORY CONTINUES. IN CC. these humanised antibodies none of the amino acids of the non-human		Query Match 79.8%; Score 304; DB 6; Length 408; Rest local Similarity 90.0%: Pred. No. 3.28e-189;	rvative
	<pre>Db 202 gatggaactgttaaactcctgatctattacacatcaagtttacactcaggagtcccatca 261</pre>	<pre>Db 262 aggttcagtgggcagtgggtctgggacagattattctctcaccatcagcaacctggaacct 321</pre>	<pre>3b 322 gaagatattgccacttactattgtcagcagtatagtaagcttccgtggacgttcggtgga 381</pre>	382 ggcaccaagctggaaatcaa 401 1 2y 361 GGGACCAAGCTGGAAATAAA 380	RESULT 9 DNA; 402 BP.		Rey Musculus.			ge (n)	PF 13-NOV-1990; U06615. PR 13-NOV-1989; US-433730.	PA (XOMA-) XOMA CORP.	Better	WP1; 91-1/8044/24. P-PSDB; R12359.	remove ni-1 durigen itom sample 28 Disclosure; fig 13; 107pp; English.		viral antigen. It is used in the	comprising heavy and light chains having murine v regions at C regions. The chimeric MAbs are more effective than murin	CC ICII since they have an increased compatibility in humans. The		They can also be used in diagnosis of HIV.	oc see also discos-ou and discost-os. SQ Sequence 402 BP; 108 A; 99 C; 88 G; 107 T;	Query Match 84.5%; Score 322; DB 2; Length 402;		Db 22 atgatgtcctctgctcagttccttggtctcctgttgctctgtttcaaggtaccagatgt 81

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	AD A CHAIR EXPLESSION VECUOI WAS CONSULUCIED BY JOINING
88	the Hotain variable region gene from pKW641HA3 to a vertor for chimeric human Ab H chain expression using
3 S &	the synthetic DNAs given in 06439 and 063440. Sequence 408 BP; 102 A; 102 C; 94 G; 110 T;
Qu Be Ma	Query Match 79.8%; Score 304; DB 11; Length 408; Best Local Similarity 90.0%; Pred. No. 3.28e-189; Matches 342; Conservative 0; Mismatches 38; Indels 0; Gaps
Db Qy	25 atgatgtcctctgctcagttccttggtctcctgttgctctgtttcaaggtaccagatgt 84
Dp Oy	85 gatatocagatgacacagactgcatcctcctgcctgcctctctgggagacagagtcacc 144
d y	atcagttgcagtgcaagtcaggacattagtaattatttaaactggtatcaacagaaacca
g &	205 gatggaactgttaaactcctgatcttttactcatcaaatttacactcgggagtccatca 264
Db Qy	265 aggttcagtggcggtgggtccgggaccagattattctctcaccatcagcaacctggagcct 324
oy op	325 ggagatattgccacttacttttgtcatcagtatagtaagcttccgtggacgtccggtgga 384
Db Qy	385 ggcaccaagctggaaatcaa 404
RESULT ID T	LT 12 T05313 standard; DNA; 324 BP.
K K C C C	103313; 02-FEB-1996 (first entry) B-cell lymphoma CH12 IgM light chain DNA. Monoclonal antibody; MAb; SCH94.03; hybridoma; central nervous system; CNS; demyelination; multiple sclerosis; neural disease; therapeutic;
MA SO	B-cell lymphoma; CH12; IgM; ds. Mus CH12; IgM; ds.
PD PF	MUSJOUU4-AI. 09-NOV-1995; 27-ARR-1995; UG5262. 29-ARR-1994; US-236520.
PA PI DR	(MAYO-) MAYO FOUNDATION. Miller DJ, Rodriguez M; WPI; 95-393077/50.
PT PT	Monoclonal antibodies which stimulate central nervous system re-myelinathon - are produced by hybridoma ATCC (RL 1167), for treating multiple scherois, and viral or nost-neural diseases of
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two amplified domains and a (Gly4Ser)3 linker. The amino terminus of the VL-VH fusion cassette was fused at the Sall site to the L6 light chain variable region leader peptide and the carboxy-terminus was fused directly to the hinge region of the Fc domain at the BclI site and/or to a short "helical" peptide linker to construct the bispecific CD3-L6FvIg antibody derivative. The variable regions for L6 were fused in frame to the opposite end of amplified by PCR methods. A gene fusion was constructed from the binding domains for separate targets joined by helical peptide, ; 0 Expression vector encoding bispecific fusion protein - having The VL and VH sequences of the anti-CD3 hybridoma G19-4 were Query Match 73.5%; Score 280; DB 12; Length 913; Best Local Similarity 94.3%; Pred. No. 2.05e-172; 210 T; 0; Mismatches 18; Indels 228 G; the helical linker (not included in Q81076) useful e.g. for diagnosis and treatment Example 1; Fig 11; 50pp; English. 252 A; 298; Conservative 94-250885/31. 913 BP P-PSDB; R60206. Sequence Linsley Jul 8 08:43 9/ Matches g 8 ዋ δ

ö 255 240 315 301 GAAGACATTGCCACTTACTTTTGCCAACAGGGTAACACGCTTCCGTACACGTTCGGAGGG 360 gacatccagatgacacagactacatcctcctgtctgcctctctgggagacagagtcacc 135 Gaps aggttcagtggcagtgggtctggaacagattattctctcaccattgccaacctgcaacca 196 gatggaactgttaaactcctgatctactacacatcaagattacactcaggagtcccatca 241 AGGTTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAACAACCTGGAGCAA 316 gaagatattgccacttacttttgccaacagggtaatacgcttccgtggacgttcggtgga 361 GGGACCAAGCTGGAAA 376 376 ggcaccaaactggtaa 391 526 g 셤

engineering; humanized antibody; Monoclonal antibody N10; target binding polypeptide; scFv; scFv; single chain antibody; protein secretion; FLAG; Location/Qualifiers influenza virus; neuraminidase; ss /*tag= a /note= "pelB signal sequence" W09407921-A. T 14 Q62957 standard; DNA; 831 BP. Escherichia coli; antibody 09-SEP-1994 (first entry) Anti-influenza N10 scFv Not specified sig_peptide 062957; g ð ð

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PF	24-SEP-1993; AU0491.	ď	28-MAY-1
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1 5	waying a scalie cute polypepture teglani maria tarnat binding ranian angala attachad ang mutatod to alter	11	Disclosing
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Sd	Dischante Page 41: 67nm: English.	5	detect
٤ د	June Office framment of NC10 (a monoclona) antibody that recognises	8 5	CD14 or
3 5	nn och tragalante en nett (a miniocatoura miniocat) innet recognisee influenca virue NO mentaminidaes) was extraseed in Ferbarichia	3 5	act i tot i
3 5	initianing virus (v. neuraminiladee) nas expressed in modifications of the N-terminal DelB eignal mentide directed the orby	3 5	therany
88	cont. The character of the periplasm where it became associated with the	S	Sequence
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ខ្ល	the C-terminus of scFv and used to monitor scFv during	ð.	Query Match
ပ္တင္တ	purification. Sequence 831 BP; 220 A; 197 C; 214 G; 200 T;	₩ ₩	Best Local Matches 2
ō	Query Match 72.2%; Score 275; DB 10; Length 831;	Dp	1 atg
Ma		Οy	111 70 ATG
QQ	475 gatatcgagctcacacagactacatcctccctgtctgcctctctgggagacagagtcacc 534	qq	61 agg
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Ŝ	17. ALCROTTGGRAGGGCRARGTCRAGGRAGTTRAGGGGGGTTRAGGGGGGGGGG	Ž	114 061
DP	595 gatggaactgttaaactcctgatctactacacatcaaatttacactcagaagtcccatca 654	q	181 ggc
δy	181 GATGGAACTATTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA 240	Qy	250 GGC
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3	gggaccaagcrcgagaraa	Seal	Search comple
φ	361 GGGACCAAGCTGGAAATAA 379	Job	Job time: 40
RESULT	LT 15		
0 Z	Q80294 standard; DNA; 62/ BP. O80294:		
占 :	1995 (first		
∃ ∑	Monocionai antibody 18E1Z 11ght chain. CD14 receptor; monocional antibody; 18E12; hybridoma;		
X 8	antiseptic; therapeutic; ds.		
3 =	nomo saprens. Key Location/Oualifiers		
FT	peptide		
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PF	27-MAY-1994; U05898.		

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993; US-070160. SCRIPPS RES INST

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tch RJ; 95-022719/03.

DB; R64204.

idoma cell lines produce MAb which inhibit CD14-mediated cell vation — for detecting CD14 in a sample and to inhibit the ling of LPS to CD14.

losure; Fig 5; 91pp; English.

i-human soluble CD14 receptor MAb 18E12 may be used to ett CD14 in cell samples, to inhibit binding of LPS to ett CD14 in cell samples, to inhibit binding of LPS to introduce to a cell, to inhibit cD14-mediated ivation of a cell expressing CD14 receptor, and for sepsis

139 T; 143 G; 161 C; 184 A; 627 BP;

Gaps 3; 64.0%; Score 244; DB 13; Length 627; Similarity 91.6%; Pred. No. 2.68e-147; 85; Conservative 0; Mismatches 23; Indels

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

- n.a. database search, using Smith-Waterman algorithm n.a. MPsrch_nn Mon Jul 8 08:53:55 1996; MasPar time 178.28 Seconds 768.287 Million cell updates/sec Run on:

Tabular output not generated.

(1-381) from USO8137117B.seq 381 >US-08-137-117B-28 Title:

Description: Perfect Score: N.A. Sequence:

1 ATGGTGTCCTCAGCTCAGTT......GGACCAAGCTGGAAATAAAT 381 TACCACAGGAGTCGAGTCAA......CCTGGTTCGACCTTTATTT

TABLE default Scoring table:

Gap 6

Dbase 0; Query 0 •• Nmatch STD 518261 seqs, 179750453 bases x 2 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8 9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14 15:EST15 16:EST16 17:EST11 12:EST12 13:EST13 14:EST14 15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20 21:EST20 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26 27:EST27 28:EST26 29:EST29 30:EST30 31:EST31 32:EST33 33:EST33 34:EST34 34:EST34 34:EST34 34:EST34 34:EST34 34:EST34 34:EST34 34:EST34 34:EST36 34:EST37 34:EST37 34:EST37 34:EST37 34:EST37 34:EST37 34:EST36 34:EST36 34:EST37 34:EST37 34:EST36 34:EST37 34:EST37 34:EST37 34:EST36 34:EST37 34:

Database:

110:enEST2 111:enEST3 112:enEST4 113:enEST5 114:enEST6 115:enEST7 116:enEST8 117:enEST9 118:enEST10 119:enEST11 120:enEST12 121:enEST13 122:enEST14 123:enEST15 124:enEST16 127:enEST19 95:qnEST1 96:qnEST2 97:qnEST3 98:qnEST4 99:qnEST5 100:qnEST6 101:qnEST7 102:qnEST8 103:qnEST9 104:qnEST10 105:qnEST11 106:qnSTS1 107:qnSTS2 108:qnSTS3 109:enEST1

Jul 8 08:46

128:enEST20 129:enEST21 130:enSTS1 131:enSTS2 132:enSTS3

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Mean 10.019; Variance 1.775; scale 5.646 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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A Pellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L.,
A Saudek D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R.,
A Weidman J.F., Li Y., Bednarik D.P., Gao L., Cepeda M.A.,
Coleman T.A., Collins E.J., Dimke D., Feng P., Ferrie A.,
A Fischer C., Hastings G.A., He W.W., Hu J.S., Greene J.M.,
A Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li H.,
A Meisener P.S., Olsen H., Raymond L., Wei Y.F., Wing J., Xu C.,
A Yu G.L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A.,
A Haseltine W.A., Fields C., Fraser C.M., Venter J.C.,
Thittial Assessment of Human Gene Diversity and Expression
T Patterns Based Upon 52 Million Basepairs of cDNA Sequence"; 252 253 AGTGGGTCTGGAACAGATTATTCTCTCACCATTAACAACCTGGAGCAAGAAGACATTGCC 312 364 313 ACTTACTTTTGCCAACAGGGTAACACGCTTCCGTAC-ACGTTCGGAGGGGGGGCCAAGCT 371 245 tctggatctgggacagatttcactctcaccatcagcagtctgcaacctgaagatgttgca 304 Research 932 Clopper Rd, Gaithersburg, MD 20878 Tel: 3018699056 Fax: 3018699423 Email: tdbinfo@tdb.tigr.org For clone availability, additional sequence and expression information related to this EST, 12-JAN-1995 (Rel. 42, Created)
07-SEP-1995 (Rel. 45, Last updated, Version 2)
EST100653 Homo sapiens cDNA 5' end similar to immunoglobulin kappa light chain, V region (GB:L01279) (HT:3043). Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A., Bult C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D., White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.W., Clayton R.A., Cline R.T., Cotton M.D., Earle-Hudghes J., Fine L.D., FitzGerald L.M., FitzHudy W.M., Fritchman J.L., Geoghagen N.S.M., Glodek A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle Jr P.S., Kelley J.M., Korken, Kelley J.C., Liu L.I., Marmaros S.M., Merrick J.M., MORENO-PALANOUES R.F., McDonald L.A., Nguyen D.T., Other ESTs: THC24356 Contact: Venter, JC The Institute for Genomic please contact the TIGR Database (tdbinfo@tdb.tigr.org). NCBI gi: 185 aagctcctgatctctgctgcatccaatttgcgaagtggggtcccatcaaggttcagtggc 305 acttactactgtcaacagagttncacttatgnctcggacggttggccaagggaccaaggt Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae. /organism="Homo sapiens" LT 2
HST27593 standard; RNA; EST; 393 BP. Location/Qualifiers /note="human" Homo sapiens (human) PAC DE LA PAC DEL PAC DEL PAC DE LA PAC DEL PAC DE

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Homo sapiens

ORGANISM

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ACCESSION KEYWORDS SOURCE

DEFINITION

RESULT LOCUS Wilson, R.

TITLE

AUTHORS

REFERENCE

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Tel: 3018699056 Fax: 3018699423 Best Local Similarity Homo sapiens 87 a Query Match source DEFINITION ORGANISM BASE COUNT Matches JOURNAL ACCESSION AUTHORS REFERENCE KEYWORDS FEATURES TITLE COMMENT ORIGIN RESULT SOURCE 엄 δ 셤 ö Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldher R.A.,
Bult C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D.,
A White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.W.,
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A. Glodek A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle Jr P.S.,
A. Merley J.M., Klimek K.M., Kelley J.C., Liu L.I., Marmaros S.M.,
A. Merlick J.M., MORNO-PAIANQUES R.F., McDonald L.A., Nguyen D.T.,
A. Bellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L.,
A. Saudek D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R.,
A. Golman T.A., Collins E.J., Dimke D., Ferife A.,
R. Fischer C., Hastings G.A., He W.W., Hu J.S., Greene J.M.,
A. Hudson P. Kim A., Kozak D.L., Kunsch C., Ji H., Li H.,
Meisner P.S., Olsen H., Raymond L., Wei Y.F., Wing J., Xu C.,
R. Yu G.L., Ruber J., Husper D., Fannon W.R., Rosen C.A.,
R. W. G.L., Ruber S.W., Dillon P.J., Fannon W.R., Rosen C.A., 135 gccagtcaggacattagcagttatttagcctggtatcagcaaaaaccagggaaagccct 194 195 gaactoctgatctatgttacatccactttgcagagtggggtcccatcaagnttcagcggc 254 acceagtetecatectecntgtetgeatetgtaggagacagagteacegteacttgeegg 134 ACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCCACCATCAGTTGCAGG 132 133 GCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCAGATGGAACTATT 192 13 GCTCAGTTCCTTGGTCTCTGTTGCTCTGTTTTCAAGGTACCAGATGTGATATCCAGATG 72 15 getcageteetggggeteetgetgetetggeteecaggtgeeagatgtgeeatceagttg 74 Gaps Other ESTS: EST69383 Contact: Venter, JC The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878 Tel: 3318699056 arx: 3018699423 Email: tdbinfoedb.tigr.org For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfoetdb.tigr.org). NCBI gi: 0 Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae. Length 395; Haseltine W.A., Fields C., Fraser C.M., Venter J.C.; "Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence"; 0; Mismatches 62; Indels 255 gntggatctgggacagctttcactctcaccatcagcagcctgcagc 300 BP; 87 A; 110 C; 95 G; 96 T; 7 other; DB 114; Pred. No. 0.00e+00; /organism="Homo sapiens" Score 165; Location/Qualifiers /note="human" 43.3%; 224; Conservative . >395 Homo sapiens (human) Best Local Similarity Sequence 395 Unpublished. Query Match source 611210 73 **PRNA** Matches 75 염 ã g P à g ð ð 원 8

Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L.,
Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R.,
Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A.,
Coleman, T.A., Collins, E.-J., Dinke, D., Feng, P., Ferrie, A.,
Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M.,
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Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C.,
Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldher, R.A.,
Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
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FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr.P.S.,
Kelley, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T.,
Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Initial Assessment of Human Gene Diversity and Expression Patterns For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database ö immunoglobulin kappa Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; 75 acceagtetecatectecnitytetgeatetgtaggagacagagteacegteacitgeegg 134 73 ACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACCATCAGTTGCAGG 132 Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; 15 gctcagctcctggggctcctggctctggctcccaggtgccagatgtgccatccagttg 74 13 GCTCAGTTCCTTGGTCTCCTGTTGCTCTGTTTTCAAGGTACCAGATGTGATATCCAGATG 72 06-SEP-1995 Gaps Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. ö human primer=M13 Reverse library=Human Lymphoid tíssue. Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C. Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Length 395; Indels 7 others Based Upon 52 Million Basepairs of cDNA Sequence end similar to 돐 ight chain V region (GB:K02096) (HT:3819). 62; Score 165; DB 70; Pred. No. 0.00e+00 Contact: Venter, JC The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878 0; Mismatches 96 t /organism="Homo sapiens" CDNA 5' Location/Qualifiers 95 g Email: tdbinfo@tdb.tigr.org /note="human" (tdbinfo@tdb.tigr.org) T29112 395 bp EST69384 Homo sapiens Other ESTs: EST69383 43.3%; 78.3%; 110 c (bases 1 to 395) 224; Conservative Unpublished (1995) <1..>395 NCBI gi: 611210 δ

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gaactcctgatctatgttacatccactttgcagagtggggtccatcaagnttcagcggc 254 193 AAACTCCTGATCTACTACATCAAGATTACACTCAGGAGTCCCATCAAGGTTCAGTGGC 252

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253 AGTGGTCTGGAACAGATTATTCTCTCACCATTAACAACCTGGAGC 298

255 gntggatctgggacagctttcactctcaccatcagcagcctgcagc 300

අු à TZ/581 288 bp mRNA EST 06-SEP-1995 EST100107 Homo sapiens CDNA 5' end similar to immunoglobulin kappa light chain gene V(I) region (HT:3862).

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RESULT LOCUS

DEFINITION

ACCESSION

KEYWORDS

SOURCE

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarihini; Hominidae; Homo. 1 (bases 1 to 288)

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

human primer=M13 Reverse library=Human Pancreas.

Homo sapiens

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Fax: 3018699423 Email: tdbinfo@tdb.tigr.org For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database

(tdbinfo@tdb.tigr.org)

NCBI gi: 609679

source

FEATURES

/organism="Homo sapiens" Location/Qualifiers

/note="human"

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The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878 Tel: 3018699056

Contact: Venter, JC Unpublished (1995)

JOURNAL

TITLE

Based Upon 52 Million Basepairs of cDNA Sequence

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133 GCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCAGATGGAACTATT 192 chain V region, rearranged (HT:3785) LT 9 HST27721 source 1-288 BASE COUNT JOURNAL **PRNA** EST. FEATURES TITLE COMMENT ORIGIN g 셤 g g δ 염 ð δ ð Š Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weldman, J.E., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J., Dinke, D., Feng, P., Ferrie, A., Erscher, C., Hastings, G.A., He, W.-M., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Meissner, P.S., Olaen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldher, R.A.,
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Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nquyen, D.T.,
Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., 5; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 288) T27721 288 bp mRNA EST 06-SEP-1995 EST13641 Homo sapiens CDNA 5' end similar to immunoglobulin light aaggtcctgatctacggtgcatccganttggaaacaggggtcccatcaaggttcagtgga 245 66 acccagictccatcctcctgintgcatcintaggaggcagagicaccatcactigccag 125 gcgagtcaggacattcgcaactatttaaattggtaccagcaaaaaccagggaaagcccct 185 133 GCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCAGATGGAACTATT 192 193 AAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCAAGGTTCAGTGGC 252 geteageteetggggeteetgetgetetggeteteaggtgeeagatgtgacatecagatg 65 13 GCTCAGTTCCTTGGTCTCCTGTTGCTCTTTTCAAGGTACCAGATGTGATATCCAGATG 72 Gaps and expression information related to this EST, please contact the TICR Database (tdbinfo@tdb.tigr.org). NCBI gi: 609679 2; Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Length 288; Indels human primer=M13 Reverse library=Human Testis. 253 AGTGGG-TCTGGAACAGATTATTCTCT-CACCATTAACAACCT 293 246 agtgggatctggggcaaagtttacttttcaccatcagcagcct 288 BP; 66 A; 81 C; 71 G; 67 T; 3 other; Score 146; DB 127; Pred. No. 9.92e-265; 0; Mismatches 63; chain V region, rearranged (HT:3785). /organism="Homo sapiens" Location/Qualifiers /note="human" 38.3%; 77.0%; = = = 218; Conservative Homo sapiens Best Local Similarity T27721 Sequence 288 Query Match ∞ source DEFINITION ORGANISM Matches 9 126 186 mRNA ACCESSION REFERENCE AUTHORS KEYWORDS SOURCE

Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C. Initial Assessment of Human Gene Diversity and Expression Patterns Email: tdbinfoetdb.tigr.org For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database Based Upon 52 Million Basepairs of cDNA Sequence Unpublished (1995) The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878 Tel: 3018699056 (tdbinfo@tdb.tigr.org). Other ESTs: THC24356 Contact: Venter, JC Fax: 3018699423

Location/Qualifiers NCBI gi: 609819

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end similar to immunoglobulin light o/-SEY-1995 (Rel. 45, Last updated, Version 2) EST13641 Homo sapiens cDNA 5' end similar to in 12-JAN-1995 (Rel. 42, Created) 07-SEP-1995 (Rel. 45, Last upd

Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae Homo sapiens (human)

Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A., Bult C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D.,

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High quality sequence stops: 218 Email: est@watson.wustl.edu Ξ source ORGANISM BASE COUNT TITLE JOURNAL Matches 192 AUTHORS REFERENCE FEATURES RESULT COMMENT 용 g g ð 쉽 δ ð δ 4; RA White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.W.,
Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D.,
R. FitzGerald L.M., FitzHugh W.M., Fritchman J.L., Geoghagen N.S.M.,
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R. Kelley J.M., Klimek W.K., Kelley J.C., Liu L.I., Marmaros S.M.,
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Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li H.,
R. Meissner P.S., Olsen H., Raymond L., Wei Y.F., Wing J., Xu C.,
Xu G.L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A.,
R. Haseltine W.A., Fields C., Fraser C.M., Venter J.C.;
R. Initial Assessment of Human Gene Diversity and Expression
R. Patterns Based Upon 52 Million Basepairs of CDNA Sequence"; 125 gcaagtnagagcattagcagctatttaanttggtatcagcagaaaccagggaaagcccct 184 human clone=134292 library=Soares placenta Nb2HP vector=pT7T3D 65 acccagintccatcgicctgintgcatcintaggagacagagicaccaicactigccgg 124 73 ACACAGACTACATCCTCCCTGTCTGCCTCTGGGAGACAGAGTCACCATCAGTTGCAGG 132 GCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCAGATGGAACTATT 192 64 13 GCTCAGTTCCTTGGTCTCCTGTTGCTCTTTCAAGGTACCAGATGTGATATCCAGATG 72 28-APR-1995 Gaps R31204 451 bp mRNA EST 28-APR-1995 yh62a07.rl Homo sapiens cDNA clone 134292 5' similar to gb:X00965_cds1 1G KAPPA CHAIN PRECURSOR V-I REGION (HUMAN);. Fax: 3018699423 Email: tdbinfo@tdb.tigr.org For clone availability, Other ESTs: THC24356 Contact: Venter, JC The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878 Tel: 3018699056 additional sequence and expression information related to this EST, 5 geteageteetgggggeteetnetaetntggeteegaggtgeeagatgtaacateeagatg please contact the TIGR Database (tdbinfoetdb.tigr.org). NCBI gi: 609819 4; 36.2%; Score 138; DB 127; Length 288; 76.2%; Pred. No. 1.80e-246; Indels 252 -CAGTGGG-TCTGGA-ACAGATTATTCTCTCACCATTAACA 289 245 gcagtgggatctggggacagattnanttnaccatcagca 285 BP; 65 A; 75 C; 70 G; 67 T; 11 other; 0; Mismatches 63; /organism="Homo sapiens Location/Qualifiers /note="human" Matches 214; Conservative <1..>288 Best Local Similarity = = = R31204 Sequence 288 Unpublished. Query Match RESULT 10 source DEFINITION mRNA 133 ACCESSION KEYWORDS SOURCE rocus

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Eucaryotae; Wetazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo. 1 (bases 1 to 451) cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3vector. Library went through one round of normalization. Library Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Rucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 constructed by Bento Soares and M.Fatima Bonaldo. Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine The WashU-Merck EST Project Unpublished (1995) Fax: 314 286 1810 Homo sapiens Wilson, R.

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. 9 others 116 t /organism="Homo sapiens" Source: IMAGE Consortium, LLNL 117 g Location/Qualifiers /clone="134292" /note="human 110 c NCBI gi: 787047 1..451 99 a

Gaps ä Score 124; DB 42; Length 451; Pred. No. 1.01e-214; 0; Mismatches 33; Indels Query Match 32.5%; Best Local Similarity 82.6%; 161; Conservative

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REFERENCE AUTHORS

US-08-137-117B-28 rat

Qy 133 GCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCAGATG-GAACTAT 191	Db 203 tcagctcctgatctatcttacatctaaattgcaaagtggggtcccatctagggttcagt 262	Qy 192 TAAACTCCTGATCTACACATCAGATTACACTCAGGAG-TCCCATCAGG-TTCAGT 249	Db 263 gggcagtggg 272 Qy 250 GG-CAGTGGG 258	TIMS	ΙÏ	z		<pre>1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGCCCGCCCTTTTTTTTT</pre>	digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares	and M.Fatima Bonaldo. ORGANISM Homo sapiens	Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Wertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhin; Hominidae; Homo.	REFERENCE 1 (bases 1 to 243) AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Lennon, G., Marra, M.,	Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaski, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson R.	TITLE The WashU-Merck EST Project JOURNAL Unpublished (1995)	Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108	Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu	Source: IMAGE CONSOTIUM, LAND This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.		Source: IMAGE Consortium, LLNL This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. NCBI gi: 895075 FEATURES Location/Qualifiers /organism="Homo sapiens" /clone="Incata" /clone="Incata"	rce NT	ES ource OUNT	ES ource OUNT	- 2 68 - 1
R49881 335 bp mRNA EST 18-MAY-1995	19.rl Homo sapiens cDNA clone 152681 5' simila 1965_cds1 IG KAPPA CHAIN PRECURSOR V-1 REGION		human clone=152681 library=Soares breast ZNbHBst vector=pT713D (Pharmacia) with a modified polylinker host=bH10B (ampicillin resistant) primer=M1RPI Rsitel=Not I Rsite2=Eco RI Adult female. let strand cDNA was primed with a Not I - oligo(dT) primer [5"			Soares and M.katima Bonaido. Homo aspiens Fhylarvotae: Metazoa: Elmetazoa: Rilateria: Coelomata:	Deuterostomia; Chordata; Vertebrata; Cathostomata; Osteichthyes; Sarcopterygii; Chordata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 335) Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,	Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.	The WashU-Werck EST Project Unpublished (1995)	Contact: Wilson RK WashU-Merck EST Project Washindton University School of Medicine	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810	Email: est@watson.wustl.edu High quality sequence stops: 235 <arrangle 11n1.<="" compartium="" td=""><td>This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.</td><td></td><td></td><td>31.5%;</td><td>31.5%; 78.0%; vative</td><td>31.5%; Score 120; DB 47; Length 335; 78.0%; Pred. No. 1.05e-205; vative 0; Mismatches 51; Indels 4; Gaps getectgctactctggctccgaggtgccagatgtgacatccagatg 82 </td><td>31.5%; Score 120; DB 47; Length 335; 78.0%; Pred. No. 1.05e-205; vative 0; Mismatches 51; Indels 4; Gaps gctcctgctactctggctccgaggtgccagatgtgacatccagatg 82 </td><td>31.5%; Score 120; DB 47; Length 335; 78.0%; Pred. No. 1.05e-205; vative 0; Mismatches 51; Indels 4; Gaps gctcctgctactctggctccgaggtgccagatgtgacatccagatg 82 </td><td>; Score 120; DB 47; Length 335; ; Pred. No. 1.05e-205; 0; Mismatches 51; Indels 4; Gaps gctactctggctccgaggtgccagatgtgacatccagatg 82 </td><td>Ist strand CDNA was primed with a Not I — oligo(df) primer [5, TGTTACCAATCTGAAGTGGGGGGGCGCCCTTTTTTTTTT</td></arrangle>	This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.			31.5%;	31.5%; 78.0%; vative	31.5%; Score 120; DB 47; Length 335; 78.0%; Pred. No. 1.05e-205; vative 0; Mismatches 51; Indels 4; Gaps getectgctactctggctccgaggtgccagatgtgacatccagatg 82	31.5%; Score 120; DB 47; Length 335; 78.0%; Pred. No. 1.05e-205; vative 0; Mismatches 51; Indels 4; Gaps gctcctgctactctggctccgaggtgccagatgtgacatccagatg 82	31.5%; Score 120; DB 47; Length 335; 78.0%; Pred. No. 1.05e-205; vative 0; Mismatches 51; Indels 4; Gaps gctcctgctactctggctccgaggtgccagatgtgacatccagatg 82	; Score 120; DB 47; Length 335; ; Pred. No. 1.05e-205; 0; Mismatches 51; Indels 4; Gaps gctactctggctccgaggtgccagatgtgacatccagatg 82	Ist strand CDNA was primed with a Not I — oligo(df) primer [5, TGTTACCAATCTGAAGTGGGGGGGCGCCCTTTTTTTTTT

BASE COUNT

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Query Match 31.5%; Best Local Similarity 78.0%; Matches 195; Conservative

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4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	133 g 122 t	28.3%; Score 108; DB 4: larity .73.0%; Pred. No. 8.10e-	0; Mismatches 65; Indels 1; Gap	Db 5 gngcaagtcagaccattagcgactatttaaattggtatcagcagaaaccagggaaagccc 64	131 GGGGAAGTCAGGACATTAGCAGTTATTAAACTGGTATCAGCAGAAACCAGATGGAACTA	Db 65 ctaaactgctgatctattctgcgtccagtttgcaaagtggggtcccccaaggttcagtg 124	Db 125 gcagtggatctgggacagatttcactctcatcatcaccagtctgcaacctgaagattttg 184	Qy 251 GCAGTGGGATTGGAACAGATTATTCTCTCACCATTAACAACCTGGAGCAAGAAGACATTG 310	Db 185 ccacttattattgtcagcagagttacagtatccctacacttttgggccagggaccaaa 244	245 qtgq 248	Qy 370 CTGG 373	RESULT 14	ij	ACCESSION R69532 KFWAGRRS FST.		<pre>(Prarmacia) With a modified polylinker host-bullub (ampliting resistant) primer=MI3RPl Reitel=Not I Reite2=Eco RI Adult female. let etrand cNN ass primed with a Not I = plinc(dT) primer [5].</pre>	TOTACCARTCCAACCCACCCCCCCTTTTTTTTTTTTTTTT	digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round	of normalization to a Cot = 230 . Library constructed by Bento Soares and M.Fatima Bonaldo.	ORGANISM Homo sapiens Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;	Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcontervoii: Choanata: Tetranoda: Amniota: Mammalia: Theria:	Eutherial Archorta; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 463)	Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,	Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.	TITLE The WashU-Merck EST Project COUNTIAL Unpublished (1995)		Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 261800	Fax: 314 286 1810
	cagatg	13 GCTCACTTCCTTGGTCTCCTGTTTTCAAGGTACCAGATGTGATATCCAGATG 72	90 acccaqtctccatcctncctgtctgcttctgtgggggacgggggcaccatcacttgcogg 149	73 ACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACCATCAGTTGCAGG 132	150 gcaagtcagagcattagcaactatgtaaattngtatcagcagaaaccagggagagaccct 209	133 GCAAGTCAGGACATTAGCAGTTATTAAACTGGTATCAGCAGAACCAGTGGAACTATT 192 210 aagctcctgatct 222		13	US R28232 503 bp mRNA EST 25-APR-1995 INITION yh57e08.rl Homo sapiens CDNA clone 133862 5' similar to qb:L12106 IG KAPPA CHAIN V-I REGION (HUMAN);	R28232 R28232 WORDS EST.		obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'	AACTGGAAGAATTGCGGCCGCAGGAATTTTTTTTTTTTT	t and clothed into the Not 1 and ECO A1 stees of the modified pills vector, Library went through one round of normalization. Library constructed by Rento Scares and M Estima Runaldo.	RCANISM Homo sapiens	Eucaryotae, Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 these 1 + 503		Parsons, J., Rikkin, L., Rohlfing, T., Soares, W., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and	Wilson, R. ITLE The WashU-Werck EST Project	NOTIONAL Unpublished (1995) WENT	Contact: Wilson RK Washil-Merck EST Project	Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108	rak: 519 200 1010 Email: estëwatson.wustl.edu	High quality sequence stops: 282 Source: IMAGE Consortium, LLAN	This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.	NCBI gl: 784367 Location/Qualifiers	<pre>source 1503 /organism="Homo sapiens" /clone="133862"</pre>	/note≕"human"

ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

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DEFINITION

ACCESSION KEYWORDS SOURCE

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310 ctqaaqattttqc 322 Sequence 332 BP; Job time: 185 secs source mRNA 셤 g 원 쉱 ð 음 ð ð 음 ò ð ð ---Source: IMAGE Consortium, LINL This clone is available royalty-free through LINL ; contact the !MAGE Consortium (info@image.llnl.gov) for further information. 130 ctctcctgcagggccagtcagactgtgagcttgaatttagcctggtaccagcagaaacct 189 ggccaggctcccaggntcctcatctatggtgcatccaccagggccactggtatcccagcc 249 181 GATGGAACTATTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA 240 aggttcagtggcagtgggtctgggacagagttctttctcaccatcagcagcctgcagcct 309 241 AGGTTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAACAACCTGGAGCAA 300 11 atggaagccccagcgcacttnctcttcctcctgctactctggctnccagatattactgga 70 Gaps Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A., Bult C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D., White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.W., Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., FitzGerald L.M., FitzKudy W.M., Fritchman J.L., Geoghagen N.S., Glodek A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle Jr P.S., Kelley J.M., Klimek K.M., Kelley J.C., Liu L.I., Marmaros S.M., 09-JAN-1995 (Rel. 42, Created)
08-SEP-1995 (Rel. 45, Last updated, Version 2)
EST77181 Homo sapiens cDNA 5' end similar to immunoglobulin kappa light chain, V region (GB:M29469) (HT:3066). <u>:</u>-Theria; Eutheria; Primates; Haplorhin; Catarrhini; Hominidae Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Score 107; DB 53; Length 463; Indels 6 others Pred. No. 1.37e-176; 0; Mismatches 109; 114 t /organism="Homo sapiens"/clone="155249" High quality sequence stops: 394 301 GAAGACATIGCCACTIACTITIGCCAACA 329 310 gaagattttgcagtttattattgtcagca 338 standard; RNA; EST; 332 BP 115 g Location/Qualifiers est@watson.wustl.edu /note="human" 28.18; Best Local Similarity 66.6%; 125 c 219; Conservative 1..463 NCBI gi: 843049 Homo sapiens (human) = Query Match HS34210 T29342 source 1-332 BASE COUNT 190 250 Matches FEATURES

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A Merrick J.M., MORENO-PALANQUES R.F., McDonald L.A., Nguyen D.T., Rellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L., Saudek D.M., Shirley R., Smail K.V., Spriggs T.A., Utterback T.R., McGoleman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A., Coleman T.A., Collins E.J., Dimke D., Feng P., Ferrie A., Fischer C., Hastings G.A., He W.W., Hu J.S., Greene J.M., Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., IA, W. G.L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A., A Haseltine W.A., Fields C., Fraser C.M., Venter J.C., R. Initial Assessment of Human Gene Diversity and Expression T. Patterns Based Upon 52 Million Basepairs of CDNA Sequence"; Fax: 3018699423 Email: tdbinfo@tdb.tigr.org For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org). NCBI gi: Other_ESTs: THC22876 Contact: Venter, JC The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878 Tel: 3018699056 Location/Qualifiers Unpublished. 611440

70 gaaattntnttgacacagtctccagccacctgtntttgtntccaggggaaagagccacc 129 61 GATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCTCTGGGGAGACAGAGTCACC 120 9 10 atggaagccccagctcagcttctnttcctcctgctactctggctcccagataccacgga 69 1 ATGGTGTCCTCAGGTCCATGGTCCTTGGTCCTCTGTTTTCAAGGTACCAGATGT 5; Score 100; DB 118; Length 332; Pred. No. 4.69e-161; Indels 0; Mismatches 103; = 26.2**%**; 66.5**%**; 208; Conservative Best Local Similarity Query Match Matches

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn Mon Jul 8 08:57:18 1996; MasPar time 281.30 Seconds 1034.412 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-137-117B-30 (1-411) from US08137117B.seq Description: Perfect Score: Title:

1 ATGAGAGTGCTGATTCTTT......CCTCAGTCACCGTCTCCTCA 411 TACTCTCACGACTAAGAAA......GGAGTCAGTGGCAGAGGGG N.A. Sequence: Comp:

TABLE default Gap 6 Scoring table:

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Listing first 45 summaries Minimum Match 0% Post-processing:

embl-new11 Database:

1:BCT 2:FUN 3:INV1 4:INV2 5:INV3 6:MAM 7:ORG 8:PLN 9:PR11 10:PR12 11:PR13 12:PR01 13:PR02 14:R0D 15:SYN 16:UNC 17:VRT 18:VIR

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Database:

genbank-newll 72:BCT1 73:BCT2 74:INV1 75:INV2 76:WAM 77:PHG 78:PLN 79:PRL1 80:PRL2 81:PRL3 82:ROD 83:STR 84:SYN 85:UNA BC:NLL 87:VRT .

Database:

88:part1

Mean 10.250; Variance 3.740; scale 2.741 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

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Description		Mouse Ig rearranged H	Mouse Ig rearranged H	Mouse mRNA for immuno	Mus musculus BALB/c/J	Mouse Iq rearranged H	Ig	Iq rearranged	sculus mRNA fo	Mus musculus mRNA for	Mus musculus germline			Mouse Ig active heavy	Ιg	Mouse Ig rearranged g	ıscn		lus mRNA fo	culus (BALB/c)	Mouse Ig rearranged h			Mus musculus rearrang	Mouse Ig active mu-ch		Mus musculus Ig heavy	rearran	Mouse IgG-2a anti-p-a	Synthetic construct c	immunoglobulin heavy	sculus ant	Ig family	Mouse IgG-1 anti-p-az	Mus musculus immunogl	/H=anti-hu	musculus Ig	ä		M.musculus mRNA (L20-	Mouse IgG-1 anti-p-az	Mouse Ig gamma-chain	ig	nius m	M.musculus mRNA for i	מטש פוון וויספווש פוו
a		MUSIGHDQA	MUS I CHDOB	MMI GVHR2	MMU05284	MUS I GHDQC	MUSIGHXX	MUS I GHAAC	MUSOHP138G	MUSOHP 7D7G	MUSIGHNUL1	MUS I GHGK	MUSICLAM	MUS I CHNOH	MUSIGHXY	MUS I GHAAO	MUS1GG4014	MUSIGHJY	MUSOHP57G	MMRNA246	MUS I GHAAGA	MUS I GHACW	MUSOHP1E9G	MUSIGHNUL	MUS I GHDS	MM16690	MMU16690	MMI GAM32	_				,	_			MM1 6687	_		MMIGH11	MUSIGHZX	MUS I GHAAX	MUSIGHZY	MMVHMRB9	MMRNAIVHC	MIS TOME 7 B
DB	I	99	99	54	54	99	99	99	57	23	99	26	26	26	26	26	26	26	21	54	96	99	21	26	99	14	82	23	26	61	59	55	26	26	54	29	14	85	29	23	26	99	26	55		
Length	,	408	399	450	417	402	460	485	358	358	434	492	357	402	470	503	702	351	358	348	342	348	358	505	439	417	417	484	342	826	342	339	408	342	351	328	405	405	288	318	336	294	318	354	340	428
Query Match	-	80.3	78.6	17.6	76.4	76.2	74.7	72.3	70.3	69.1	69.1		67.9	•	66.2	•	66.2		62.9	•	64.5	64.0		63.0		62.3			-	61.8	-	60.3		59.6		•			-				57.9	•		
Score	- 1	330	323	319	314	313	307	297	289	284	284	282	279	274	272	272	272	271	271	568	265	263	262	259	257	256	256	255	254	254	252	248	248	246	243	242	241	241	240	240	240	239	238	238	237	227
Result No.		-	7	m	4	2	9	7	∞	6	10	11	12	13	14	15	16	11	18	19	70	21	22	23	24	52	56	27	28	29	99	31	32	33	34	32	36	37	38	39	40	41	42	43		

ALI GNMENTS

IUSICHDQA 408 bp mRNA ROD 28-APR-1995	Mouse Ig rearranged H-chain mRNA V-region, 5' end of cds. L20961	V-region; anti-HIA antibody; antibody;	immunoglobulin heavy chain; monoclonal antibody; processed gene.	Mus musculus (strain BALB/c, sub species domesticus) male adult	hyperimmunized spleen cDNA to mRNA.	Mus musculus
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RESULT LOCUS	DEFINITION ACCESSION	KEYWORDS		SOURCE		ORG

FEATURES

COMMENT

JOURNAL MEDLINE

REFERENCE AUTHORS

TITLE

US-08-137-117B-30.rgc

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US-08-137-117B-30.rge

	Qy 361 ACTAGGGCTATGGACTAGGGAACCTCAGTCACGTCTCTCA 411 RESULT 2 LOCUS MUSIGHDQB 399 bp mRNA ROD 28-APR-1995	1-chain mRNA V-region, 5' end		hyperimmunized spleen cDNA to mRNA. ORGANISM Mus musculus		REFERENCE 1 (bases 1 to 399) AUTHORS Iwasaki,Y., Takabatake,H., Shinji,T., Monestier,M. and Ferrone,S. TITLE Structural profile of idiotype, anti-idiotype and		JOURNAL Eur. J. Immunol. 24 (11), 28/4-2881 (1994) MEDLINE 95045941 COMMENT NCBI gi: 309346		/organism="Mus musculus" /strain="BALD/c" /sub species-"domesticus"	/cell type="hybridoma" /dev stage="adult"	/sequenced_mol="cDNA to mRNA" /sex="male"	ď	/standard name="anti-HLA-DQ3 monoclonal antibody" /note="NCBI gi: 309347" /nodqn erart-1	/product="immunoglobulin heavy chain" /translation="MRVLILIMLFTAFPGILSDVQLQESGPGLVKPSQSLSLTCTVTG /STISDYANWIRQFPGNKLEMGYITYSGSTSYNPSLKSRISITRDTSKNQFFLQLN	SVILEDIALII.CANMGALIIMGGGLLVIVOA exon 44381 exon 349361	exon 362399 BASE COUNT 93 a 107 c 94 g 105 t ORIGIN .	Query Match 78.6%; Score 323; DB 56; Length 399; Best Local Similarity 96.3%; Pred. No. 0.00e+00; Matches 336; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	1 atgagagtgctgattcttttgtggctgttcacagcctttcctggtatcctgtctgatgtg 60	61 cagetteaggagtegggacetggeetggtaaacetteteagtetetgteectaeetge	Db 121 actgractgctactcatcaccagtgattatgcctggaactggatccagaactgcagttcca 180
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;	Eutheria; Rodentia; Myomorpha; Muridae; Murinae. 1 (bases 1 to 408) Iwasaki, Y., Takabatake, H., Shinji, T., Monestier, M. and Ferrone, S. Structural profile of idiotype, anti-idiotype and anti-anti-idiotype monoclonal antibodies in the HIA-DQ3 antigenic	aystem Eur. J. Immunol. 24 (11), 2874-2881 (1994) 86045421	NCBI 91: 309344 Location/Qualifiers	1408 /organism="Mus musculus"	/strain="BALB/c" /sub_species="domesticus"	/cell_type="Lybridoma" /dev_stage="adult" /sequenced_mol="cDNA to mRNA"	/sex="male" /tissue_type="hyperimmunized spleen"	<143 1>408 /standard_name="anti-HIA-DQ3 monoclonal antibody"	/note="NCBI gi: 309345" /codon_start=1	/product="immunoglobulin heavy chain" /translation="MRVLILIMPETAPPGLISDVQLQESGPCLVKPSQSLSLFCTVTG Y31TSDHANWHROPEORLEMMGYTYSGSTSNNPSLKSRISTRPDFSKNOFFLOLN	SVTTEDTATYYCARLSVGLRLDYMOQGTTLTVSS" 44348	349367 368408	99 a 109 c 92 g 108 t	<pre>sry Match 80.3%; Score 330; DB 56; Length 408; st Local Similarity 92.0%; Pred. No. 0.00e+00; chee 378. Concernative 0. Mismatches 30. Indels 3. Cans 3.</pre>	ytgetgattettttgtggetgtteacageettteetggtateetgtetgatgt 60	onemujecieniiviiitoieeciojivakmuotiiitotieejalotoitoitahije 80 getteaggagtegggaeetggeetggtgaaaeetteteagtetetgteeeteaeetge 120	CTCACCTGC	21 actgicactggctactcaatcacgagrgatcatgcctggaactggatccggcagtitcca 180 	181 ggagacaaactggagtggatgggctacataacctacagtggtagtactagcaacaatcca 240 	24] tototcaaaagtogaatototatoactogagacacatocaagaaccagtototootgcaa 300 	301 ttgaattctgtgactactgaggacacagcacatattactgtgcaagatta-tcggtggg 359

Query Match 80.3%; Best Local Similarity 92.0%; Matches 378; Conservative

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BASE COUNT ORIGIN

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Db 1	181 ggaaacaaactggagtggatgggctacataacctacagtggtagcactagctacaaccca 240	***************************************	
Qy 1		64	cagetteaggagteaggaeetgae
Db 2	24] tetetcaaaagtegaatetetateaetegagacacatecaagaaceagtietteetgeag 300 	124	actgractggctactccatcac
	301 ttgaattetgtgactactgaggacacagccacatattactgtgcaaaat 349	121	121 ACTGTCACTGGCTACTCAATCAC
Qy 3		DD 184 9	ggaaataaattggaatggatggc
RESULT LOCUS	3 MMIGVHR2 450 bp RNA ROD 07-MAY-1992	Db 244 t	244 tctctcaaaagtcgaatctctatc
DEFINITION ACCESSION		Qy 241 1	241 TCTCTCAAAAGTCGAATCTCTAT
KEYWORDS SOURCE OBCANTEM	S constant region; Ig heavy chain; variable region. Nouse mouse. Tew Min microfiles	Db 304 t	304 ttgaattetgtgaetgetgaggae
Policy			tactatgctatggactactgggg
	Ver Tet Sci	Qy 361 <i>1</i>	
REFERENCE AUTHORS		5 4	
TITLE JOURNAL	Direct Submission AL Submitted (31-AUG-1987) to the EMBL/GenBank/DDBJ databases. Dr.	LOCUS	
	Francis Grant, Zymogenetics, Inc., 2121 North 35th Street, Seattle, Wa 98103, USA	ACCESSION	region (IgH) mRNA, pa: U05284
REFERENCE AUTHORS TITLE		KEYWORDS SOURCE ORGANISM	mouse. Mus musculus
JOURNAL			Eucaryotae; Metazoa; Eutheria; Rodentia; M
MEDLINE	NE 87260030 NCBI q1: 52526	REFERENCE AUTHORS	<pre>1 (bases 1 to 417) Tempest, P.R., White, P</pre>
FEATURES		TITLE	Humanized and chimerical
i		JOURNAL	Unpublished
ï		AUTHORS	Tempest, P.R.
≓ t	arnae -	JOURNAL	Submitted (21-JAN-199
3	CDS 4:.7430 /note="NCBI gi: 52527"	COMMENT	NCBI gi: 463457
	/codou_t=talt=1 /product="Vh gene product" /translation="MRVLILLCUTAFPGILSDVQLQESGPDLVRPSQSLSLTCTVTG ystrscYYWHWIROPGNKILSMAYHYSGNYDFNPSIKSRTSTPRDTSKNOFFIO.N	source	Location/Qua 1.417 /clone_lib=" /strain="BAL:
Ē	SVTAEDTATYCARGYGNYYAMDYMGQGTSVTVSSAKTTPPSVYPLA" 4152450		/organism="M
BASE COUNT ORIGIN	116 a	CDS	/cell_type="/ /tissue_type 1>417
Query Ma Best Loo Matches	Query Match 77.6%; Score 319; DB 54; Length 450; Best Local Similarity 88.8%; Pred. No. 0.00e+00; Matches 365; Conservative 0; Mismatches 46; Indels 0; Gaps 0;		/gene= 19n /note="NCBI /codon_gtart /evidenceeex
oy Oy	<pre>4 atgagagtgctgattcttttgtgcctggtcacagcctttcctggtatcctgtctgatgtg 63 </pre>		/product an chain variab /translation YSITSDYAMNWI
g vy	<pre>4 atgagagtgctgattcttttgtgcctggtcacagcctttcctggtatcctgtctgatgtg 63 </pre>		

on="MRVÍ.ILMIFTAFPGILSDVQLQESGPGLVKPSQSLSLTCTVTG MIRQFPGNKLEWMGFISYSGSTSYNPSLESRISVTRDTSKNQFFLQLY Chordata; Vertebrata; Gnathostomata; Mammalia; Myomorpha; Muridae; Mus. 7.7 immunoglobulin heavy chain complete variable partial cds. 994) Philip R. Tempest, ICOS Corporation, 22021 , WA 98021, USA unti-cytomegalovirus-gB immunoglobulin heavy bble region" acacagccacatattactgtgcaagagatatggtaac 363 15-FEB-1995 P., Buttle, M., Carr, F.J. and Harris, W.J. ized monoclonal antibodies against the numan cytomegalovirus gtcaaggaactcagtcaccgtctcctca 414 "hybridoma" e="hyperimmunized spleen" "Lambda HCMV37" \LB/c/J" "Mus musculus" ="HCMV37" I gi: 514241" rt=1 xperimental mRNA alifiers

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Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
1 (bases 1 to 402)
1 wasaki,Y., Takabatake,H., Shinji,T., Monestier,M. and Ferrone,S.
Structural profile of idiotype, anti-idiotype and
anti-anti-idiotype monoclonal antibodies in the HIA-DQ3 antigenic ö immunoglobulin heavy chain; monoclonal antibody; processed gene Mus musculus (strain BALB/c, sub_species domesticus) male adult 141 TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACACCAAGAACCAGTTCTTCCTACAG 300 61 cagetteaggagtegggacetggcetggtgaaacetteteagtetetgteceteaeetge 120 121 actgtcactggctactcaatcaccagtgattatgcctggaactggatccggcagtttcca 180 tctctcgaaagtcgaatctctgtcactcgagacacatccaagaaccagttcttcctgcag 300 1 ATGAGAGTGCTGATTCTTTTGTGGCTGTTCACAGCCTTTCCTGGTATCCTGATGTG 60 MUSIGHDQC 402 bp mRNA ROD 28-APR-1995 Mouse Ig rearranged H-chain mRNA V-region, 5' end of cds. Gaps Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; ., Score 314; DB 54; Length 417; Pred. No. 0.00e+00; 0; Mismatches 16; Indels SVTTEDTATYYCANMITTSAYWYFDVWGAGTTVTVSS: Eur. J. Immunol. 24 (11), 2874-2881 (1994) 95045941 V-region; anti-HLA antibody; antibody; /strain="BALB/c" /sub_species="domesticus" /cell_line="S01" 114 hyperimmunized spleen cDNA to mRNA organism="Mus musculus" cell_type="hybridoma" /evidence=experimental Location/Qualifiers Б 86 /gene="IgH" 55..417 /gene="IgH" Query Match 76.4%; Best Local Similarity 95.4%; 111 c 330; Conservative 309348 1..402 Mus musculus NCBI gi: 94 L20957 system sig_peptide mat_peptide S source DEFINITION ORGANISM REFERENCE AUTHORS TITLE BASE COUNT 241 Matches JOURNAL MEDLINE ACCESSION FEATURES KEYWORDS COMMENT RESULT SOURCE ORIGIN 용 음 ð 염 요 염 S g ð ð ð à

/product="immunoglobulin heavy chain" /translation="MRVLILIMLFTAFPGLLSDVQLQESGPGLVRPSQSLSLTCTVTG YSITSDYAMNWIRQFPGNKLEMMGYISYSGSTGYNPSLKSRISITRDTSKNQFILQLN /standard name="anti-HLA-DQ3 monoclonal antibody' /tissue_type="hyperimmunized spleen" SVTTEDTATYYCARFYDGFDYWGQGTTLTVSS" /sequenced_mol="cDNA to mRNA" /sex="male" ų 105 /note="NCBI gi: 309349" Б 'dev_stage="adult" 93 /codon start=1 111 c 44..348 349..359 360..402 1..>402 93 BASE COUNT exon CDS exon ORIGIN

ö Gaps ; 0 Length 402; 0; Mismatches 17; Indels Score 313; DB 56; Pred. No. 0.00e+00; Query Match 76.2%; Best Local Similarity 95.1%; 330; Conservative Matches

cagetteaggagtegggaeetggeetggtgagaeeeteteagtetetgteeeteaeetge 120 9 9 1 ATGAGAGTGCTGATTCTTTGTGGCTGTTCACAGCCTTTCCTGGTATCCTGTCTGATGTG 1 atgagagtgctgattcttttgtggctgttcacagcctttcctggtctcctgtctgatgtg 61 61 셤 ð à

actgicactggctactcaatcaccagigatiatgcctggaaciggatccggcagittcca 180 121 g ð 240 181 음 Š

300 241 TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTCCTACAG 300 tegeteaaaagtegaatetetateaetegagaeaacaeteeaagaaeeagtteateetgeag 241 염 ò

301 ttgaattctgtgactactgaggacacagccacatattactgtgcaag 347 음 δ

Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA C-region; immunoglobulin gamma-chain; immunoglobulin heavy chain; Theria; Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Mouse Ig rearranged gamma-chain mRNA, clone AN02g. M19894 J03832 IRNA I 460 bp processed gene Mus musculus MUSIGHXX 9 DEFINITION ORGANISM ACCESSION KEYWORDS SOURCE Locus

Unpublished (1988) Stanford U., Chem. Dept., Stanford CA 94305 2 (bases 55 to 460) Eutheria; Rodentia; Myomorpha; Muridae; Murinae (bases 1 to 54) Rule, G.S. JOURNAL REFERENCE AUTHORS TITLE REFERENCE AUTHORS

Leahy, D.J., Rule, G.S., Whittaker, M.M. and McConnell, H.M. Sequence of 12 monoclonal anti-dimitrophenyl spin-label anti-

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Gaps

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301 tectattectatgetatggaetactggggteaaggaaceteagteaeegteteetea 357 NCBI gi: 90 Phone: D12734 mat peptide Query Match source DEFINITION ORGANISM Matches BASE COUNT JOURNAL MEDLINE 241 355 REFERENCE AUTHORS ACCESSION KEYWORDS SCOS FEATURES SOURCE g à 쇰 염 ŏ ð /codon_start=1 /product="1g gamma chain precursor" /translation="DVQLQESGPGLVRPSQSLSLTCTVTGYSITSYSAMNWIRQFPGN RIEWMGYISYSGGTGYNPSLKSRISITRDTSRNQFFLQLNSVTTEDTATYYGSRGSSY Ig gamma chain; steroid specific antibody; variable region. Mus musculus (strain BALB/c) hybridoma cell line OHP138.H8.1 mRNA. Sawada, J., Mizusawa, S., Terao, T., Naito, M. and Kurosawa, Y. Molecular characterization of monoclonal anti-steroid antibodies: primary structures of the variable regions of seven antibodies ö specific for 17alpha-hydroxyprogesterone or 11-deoxycortisol and 55 GATGTGCAGCTTCAGGAGTCGGGACCTGTCTGGTGAAGCCTTCTCAGTCTCTGTCCCTC 114 61 acctgcactgtcactggctactcaatcaccagttattctgcctggaactggatccggcag 120 121 tttccaggaaatagactggagtggatgggctacataagctacagtggtggcactggctac 180 aacccatctctcaaaagtcgaatctctatcactcgagacacatccaagaaccagttcttc 240 11-NOV-1992 Gaps 1 gatgtgcagcttcaggagtcgggacctggcctggtgaaaccttctcagtctctgtccctc Eukaryota; Animalia; Chordata; Mammalia; Rodentia; Muridae. .; 0 Score 289; DB 57; Length 358; Pred. No. 1.20e-288; Submitted (27-JUL-1992) to DDBJ by: Jun-ichi Sawada 0; Mismatches 34; Indels MUSOHP138G 358 bp mRNA ROD Mus musculus mRNA for Ig gamma chain precursor. Ig gamma chain; steroid specific antibody; National Institute of Hygienic Sciences 'note="VDJ region (1-358)" 35 'product="Ig gamma chain" their pH-reactivity profiles Mol. Immunol. 28, 1063-1072 (1991) organism="Mus musculus" Dept. of Biochem. and Immunochem /note="NCBI gi: 220533" Location/Qualifiers б SYAMDYWGQGTSVTVSS" 03-3700-1141 x240 8 /codon_start=1 03-3707-6950 70.3%; Setagaya, Tokyo 158 99 c (bases 1 to 358) 323; Conservative <1..>358 |-18-1 Kamiyoga 1..358 220532 Best Local Similarity Mus musculus g1: 92017897 87 Phone: D12726 NCBI mat peptide Query Match source DEFINITION ORGANISM BASE COUNT 181 Matches AUTHORS TITLE ACCESSION MEDLINE REFERENCE JOURNAL SGS KEYWORDS FEATURES SOURCE ORIGIN

135 AACCCATCTCTCAAAAGTCGAATCTCTATCACTCGGACACCATCCAAGAACCAGTTCTTC 294

ctgcagttgaattctgtgactactgaggacacagccacatattactgttcaagaggatct 300

295 CTACAGTTGAATTCTGTGACTACTGGGGACACGTCCACATATTACTGTGCAAGATCCCTA 354

11-NOV-1992 MUSOHP7D7G 358 bp mRNA ROD Mus musculus mRNA for Ig gamma chain precursor.

Ig gamma chain; steroid specific antibody; variable region. Mus musculus (strain BALB/c) hybridoma cell line OHP7D7.2.3 mRNA. Eukaryota; Animalia; Chordata; Mammalia; Rodentia; Muridae. Mus musculus

Molecular characterization of monoclonal anti-steroid antibodies: primary structures of the variable regions of seven antibodies Sawada, J., Mizusawa, S., Terao, T., Naito, M. and Kurosawa, Y. (bases 1 to 358)

specific for 17alpha-hydroxyprogesterone or 11-deoxycortisol and Mol. Immunol. 28, 1063-1072 (1991) 92017897 their pH-reactivity profiles

Submitted (27-JUL-1992) to DDBJ by: Jun-ichi Sawada Dept. of Biochem. and Immunochem. National Institute of Hygienic Sciences

03-3700-1141 x240 03-3707-6950 Setagaya, Tokyo 158 1-18-1 Kamiyoga

/note="VDJ region (1-358) /organism="Mus musculus" 1..>358 Location/Qualifiers 1..358 220548

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88 t 82 g YYAMDYWGQGTSVTVSS" ပ 86

5 Gaps 2; Length 358; Indels 0; Mismatches 30; Pred. No. 6.68e-283; 69.1%; Score 284; DB 57; 91.18; 326; Conservative Best Local Similarity

1 gatgtgcagcttcagggagtcgggacctggcctggtgaaaccttctcagtctctgtccctc 60

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셤 ð 원 à 55 GATGTGCAGCTTCAGGGACCTGTCCTGGTGAAGCCTTCTCAGTCTCTGCCTC 114

61 acctgcactgtcactggctactcaatcaccagtgatcatgtctggaactgggtccggcag 120

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/product="immunoglobulin heavy chain" /translation="APPGILSDVQLQESGPCLVKPSQSLSLTCTVTGYSITSDYAWNW IRQFPGNKLEWMGYISYSGSTSYNPSLKSRISITRDTSKNQFFLQLNSVTTEGGGYDD /translation="AFFGILSDVQLQESGFCLVKPSQSLSLTCTVTGYSITSDYAWNW IRQFPGHKLEWMGYISYSGSTSYNPSLKSRISITRDTSKNQFFLQLNSVTRGGYDDAT /tranglation="AFPGILSDVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWW IRQFPGNKLEWMGYISYSGSTSYNPSLKSRISITRDTSKNQFPLQLNSVTTGGLRRRD 'product="immunoglobulin heavy chain" /product="immunoglobulin heavy chain" join(104..365,401..434) 'product="immunoglobulin heavy chain" /product="immunoglobulin heavy chain" /note="alternatively spliced exon" 'note="alternatively spliced exon" /note="alternatively spliced exon" /note="alternatively spliced exon" join(<1..10,93..365,401..434) join(<1..10, 93..371, 401..434) /note="NCBI gi: 550491" /note="NCBI gi: 550493" join (104..366, 401..434) join (104..371, 401..434) /note="NCBI gi: 550492" codon_start=1 /codon_start=1 /codon_start=1 /codon start=1 /gene="Igh" /map="12" 'gene="Igh" /gene="Igh /number=2 'number=1 /number=2 'number=2 /number=2 /map="12" /map="12 'partial partial/ 93..366 93..365 93..364 11..92 93..371 ATGTT" mat_peptide mat_peptide mat_peptide intron exon exon exon exon SBS CDS

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/translation="MRVLILIMLFTAFPGILSDVOLQESGPCLVKPSOSLSLTCTVTG YSITSDYAMNWIRQFPGNKLEWMGYISYSGSTSYNPSLKSRISITRDTSKNQFFLQLN SATTEDTATYYCARNYGSFDYWGQGTTLTVSS" join (10..52,134..144) /note="Ig mu-chain" /tissue_type="P.pneumotropica-specific anti-DNP hybridoma" join(10.52,134..>492) MUSIGHGK 492 bp DNA ROD 27-APR-1994 Mouse Ig rearranged mu-chain gene V/D/J2 region from LB8 hybridoma, anti-DNP, clone LB8-3. ö Dzierzak, E.A., Janeway, C.A.Jr., Richard, N. and Bothwell, A.L.M. Molecular characterization of antibodies bearing Id-460: The structure of two highly homologous V-H genes used to produce idiotype positive immunoglobulins
J. Immunol. 136, 1864-1870 (1986) Gaps Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae. 1 (bases 1 to 492) /note="V/D/J2-region precursor; NCBI gi: 195343" D-region; J-region; V-region; immunoglobulin heavy chain; ; 0 immunoglobulin mu-chain; processed gene. Mus musculus (strain BALB/c, sub species domesticus) P.pneumotropica-specific anti-DNP hybridoma DNA. Length 492; Indels 124 a 121 c 107 g 140 t 393 bp upstream of EcoRI site; chromosome 12. /product="immunoglobulin mu-chain" /note="Ig mu-chain V/D/J2-region" 0; Mismatches 12; Query Match 68.6%; Score 282; DB 56; Best Local Similarity 96.1%; Pred. No. 1.33e-280; /note="V/D/J2-region; putative" /sub_species="domesticus" /cell_line="LB8" /organism="Mus musculus" organism="Mus musculus" /organism="Mus musculus" /sequenced_mol="DNA" /note="Ig-mu chain" /codon start=1 438..439

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δλ	235	aacccatctctcaaaagtcgaatctctatcactcgagacacatccaagaaccagttcttc 294
d d	241	ctgcagttgaattctgtgactactgaggacacagcacatattactgtgcaagatgtccc 300
δy	295	
QQ	301	tatgatteetggtaettetegatgtetggggegeagggaecaeggteaeegteteetea 357
δλ	355	gereggactacggetategactactggggteaaggaaecteagteacetereeea 411
RESULT LOCUS DEFINI ACCESS	[TION	13 MUSIGHNOH 402 bp mRNA ROD 17-SEP-1991 N Mouse Ig active heavy-chain mRNA V-region. M44137
KEYWORDS	ORDS	
Š.	ORGANISM	Mus Euk Eut
REFE	REFERENCE AUTHORS	1 (bases 1 to 402) Caton, A.J., Stark, S.E., Kavaler, J., Staudt, L.M., Schwartz, D. and Gerhard, W.
II.	TITLE TOTIONS!	Many variable region genes are utilized in the antibody response of balb/c mice of the influenza virus a/pr/8/34 J. Tamennol 147 1675-1686 (1991)
MEDLI	MEDLINE	91349593 Specific for influenza virus A/PR/8/34 hemagglutinin.
FEATURES	Ã	NCBI gi: 195701 Location/Qualifiers ce 1402 /organism="Mus musculus"
		<pre>/strain="BALB/c" /sub species=""domesticus" /cell_line="H46-24E9" /cell_type="b-cell hybridoma" /sequenced mol="colN to mRNA"</pre>
	CDS	<pre><1.>402</pre>
BASE C	BASE COUNT ORIGIN	104 a
Ouc Ber	Query Match Best Local Matches 3	/ Match 66.7%; Score 274; DB 56; Length 402; Local Similarity 91.3%; Pred. No. 2.03e-271; Natches 303; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QQ	5	tttggtgcctgttcacagcctttcctggtatcctgtctgatgtgcagcttcaggagtcag 64
δ	11	TITGLGGCTGTTCACAGCCTTTCCTGGTATCCTGTCTGTGTGTGCAGCTTCAGGAGTCGG 76
QQ	65	gacctgacctggtgaaaccttctcagtcacttcactcacctgcactgtcactggctact 124
δy	11	GACCTGTCCTGGTGAAGCCTTCTCAGTCTCTCTCACCTGCACTGTCACTGGCTACT 136
OP	125	ccatcaccagtggttatagctggcactggatccggcagtttccaggaaacaaac
δy	137	CAATCACCAGTGATCATGCCTGGAGCTGGATCCGGCAGTTTCCAGGAACAACTGGAGT 196

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DEFINITION ACCESSION

KEYWORDS

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Qy 1 ATGAGACTCTTTTTTTGTGGCTGTTCACAGCCTTTCCTGGTATCTGTTGTGGC 60	Db 116 cagettcaggagtcaggacetggcetegtgaaacettetcagtetetgtetetcacetge 175	Db 176 totgtcactggctactccatcaccagtggttattactggaactggatccggcagtttcca 235	Db 236 ggaaacaaactggaatggatgggctacataaactacgacggtaacaataactacaacca 295 	Db 296 tetetcaaaategaatetecateactegtgacacatetaagaaccagtttteetgaag 355	Db 356 ttgaattctgtgactactgaggacacagctacatattactgtgcaagagagg-gctacg 413 	Db 414 gctattttttg-actactggggccaaggcaccactctcacagtctcctca 463 	RESULT 15 LOCUS MUSIGHAAO 503 bp mRNA ROD 26-MAR-1994 DEFINITION Mouse Iq rearranged gamma-chain mRNA, clone ANOIg.	M19893 J03832 C-region; immunoglobulin gamma-chain; processed gene. Mus musculus (strain BALB/c, sub_speci		2 (Dasses 57 to 503) Leahy, D.J., Rule, G.S., Whittaker, M.M. and McConnell, H.M. Sequence of 12 monoclonal anti-dinitrophenyl spin-label a	Dodies for NMR studies JOURNAL Proc. Natl. Acad. Sci. U.S.A. 85, 3661-3665 (1988) MEDIJINE R8734486	· •	/sub_bpc_res demost_res /cell_type="mature B cell" /sequenced_mol="cDNA to mRNA"	Signeture 50.110 COS 5755 /note="precursor; NCBI gi: 194613" /codon start=1	/product="immunoglobulin gamma-chain"
Ob 185 ggatgggctatatacactacagtggtagcactaagtacaacccatctctcaaaagtgcaa 244		297 ICTCTATCACTCGAGACACCACGAGACCGGTTCTTCCTACAGTTGATTCTGTGACTA 316 305 ctgaggacacagccacatattactgtgcaaga 336	317	MUSIGHXY 470 bp mRNA ROD 26-MAR-1. N Mouse Ig rearranged gamma-chain mRNA, clone AN03g. N M19895 J03832	NEIMONDS C-Teglon; Immunoglobulin gamma-chain; immunoglobulin neavy chain; SOURCE Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA. ORGANISM Mus musculus. Finistructa: Animalia: Chordata: Vortebrata: Mammalia: Thoria.	Extheria; Rodentia; Myomorpha; Muridae; Murinae. Extheria; Rodentia; Myomorpha; Muridae; Murinae. ATTHORS Rule, G.S. JOURNAL Unpublished (1988) Stanford U., Chem. Dept., Stanford CA 94305		JOURNAL Proc. Natl. Acad. Sci. U.S.A. 85, 3661-3665 (1988) MEDLINE 88234486 COMMENT Draft entry and computer-readable sequence [2] kindly submitted by G.Rule, 20-JUL-1988.	NCBI gi: 196227 Location/Qualifiers source /organism="Mus musculus" / strain="Mus musculus"		sig_peptide >6109 /codon_start=1 rns 56 >470	YSTTSGYWWINE PROMISE AND	/product="liminoglobuling gamma=cnain" BASE COUNT 125 a 118 c 99 g 128 t ORIGIN	Query Match 66.2%; Score 272; DB 56; Length 470; Best Local Similarity 84.9%; Pred. No. 4.00e—269; Matches 349; Conservative 0; Mismatches 59; Indels 3; Gaps 2;	Db 56 atgaaagtgttgagtctgttgtacctgttgacagccattcctggtatcctgtctgatgta 115

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/translation="MKVLSLLYLLTAIPGILSDVQLQESGPCLVKPSQSLSLTCSVTG
YSITSGYYMWHIRQFPCHKLEWMGYINYDGRNNYNPSLKNRISITRDTSKNQFFLKLK
SVTTEDTATYYCAREDDGYYIFDYWGQGSTLTVSSAKTTPPSVYPLA"
                                                                                                                                                         /product="immunoglobulin gamma-chain"
131 c 106 g 133 t
                                                                                                                               /codon_start=1
                                                                                              111.,>503
                                                                                              mat_peptide
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106 g æ 133 BASE COUNT ORIGIN

2; Gaps 2; Score 272; DB 56; Length 503; Pred. No. 4.00e-269; 0; Mismatches 63; Indels Best Local Similarity 84.2%; Matches 347; Connection

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357 ttgaagtetgtgacaactgaggacacagetacatattactgtgcaagaggatgatggt 416

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Search completed: Mon Jul 8 09:02:07 1996 Job time: 289 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn Mon Jul 8 09:02:24 1996; MasPar time 35.86 Seconds 762.194 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-137-117B-30 (1-411) from USO8137117B.seq 411 Title:

Description: Perfect Score:

1 ATGAGAGTGCTGATTCTTT.......CCTCAGTCACCGTCTCCTCA 411
TACTCTCACGACTAAGAAAA......GGAGTCAGTGGCAGAGGGGT N.A. Sequence: Comp:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 Nmatch STD 84802 seqs, 33246950 bases x 2 Searched:

Listing first 45 summaries Minimum Match 0% Post-processing:

Database:

i:parti 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 n-geneseq22

Mean 8.278; Variance 4.920; scale 1.683 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	8.03e-269	1.36e-164					2.41e-143		
Description	pPM-h1.	Fv (TU27).	Sequence of the anti-	Anti-traseolide 02/01	Monoclonal antibody 2	Sequence of the singl	VH domain of antibody	Sequence of PCR produ	Sequence of Clone 21b
ID	030756						Q06214		
DB	5	~	4	12	13	1	-	2	5
% Query e Match Length DB 1	411	720	378	714	639	836	351 1	830	798
% Query Match	100.0	64.5	62.3	62.0	61.6	61.6	57.2	52.8	51.8
Score	411	565	256	255	253	253	235	217	213
Result No.	1	2	က	4	വ	9	7	∞	0

213	51.8	798 10	044642	Fd phage clone sequen	8.10e-128
167	40.6	438 5		puc-RVh-PM11-4.	1.45e-95
29	39.4	351 7	042702	poc-kvn-rmii. Ab26.	4.41e-92
160	38.9	1		Human immunoglobulin	1.09e-90
153	37.2			VH411.	7.98e-86
153	37.2			VH415.	7.98e-86
152	37.0	1212 13		Human immunoglobulin	3,94e-85
151	36.7			Vh 71-4.	1.95e-84
151	36.7	348 7	042701	VH416.	1.95e-84
151	36.7			Human immunoglobulin	1.95e-84
149	36.3			Human immunoglobulin	4.75e-83
144	35.0	631 13		Human immunoglobulin	1.38e-79
143	34.8	348 7	042698	F105Vh.	6.78e-79
141	34.3	426 7	049154	F105 rearranged varia	1.64e-77
139	33.8	357 6		MAb GAH variable regi	3.94e-76
139	33.8	Н		Human immunoglobulin	3.94e-76
138	33.6			Anti-human RhD PAG-1	1.93e-75
132	32.1	799 13		Human immunoglobulin	2.64e-71
131	31.9			Sequence encoding the	1.29e-70
129	31.4			Sequence of the monoc	3.06e-69
129	31.4			Murine NM-01 variable	3.06e-69
127	30.9	402 10			7.24e-68
127	30.9	423 6		Anti-CD4 VH coding se	7.24e-68
123	29.9			MAb 1-3-1 variable re	4.02e-65
121	29.4	685 13		Human immunoglobulin	9.42e-64
117	28.5	363 2		Anti-human RhD FOM-A	5.12e-61
117	28.5	384 2	Q11951	Anti-human RhD FOM-1	5.12e-61
115	28.0	291 3	N50188	Sequence of human imm	1.19e - 59
111	27.0				6.31e-57
107	26.0			Anti-human RhD MAD-2	3.30e-54
107	26.0	418 13		Anti-human IL-6 chima	3.30e-54
107	26.0			Anti-human IL-6 chima	3.30e-54
105	25.5	348 7	042703	268-D.	7.48e-53
105	25.5	3314 11	058896	Humanised anti-CEA sF	7.48e-53
104	25.3	381 2	011947	Anti-human RhD FOG-B	3.56e-52

ALIGNMENTS

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has low antigenicity and contains mouse V-region complemendetermining regions Disclosure; page 127-123; 207pp; Japanese. The sequences given in Q3075-56 were used in example to the production of a human antibody which recognises human interleukin-6 receptor (IL-6R). The antibody comprises location and heavy (H) chain variable regions which were dermouse monoclonal antibody produced from the hybridoma PMI contained the plasmids pPM-K3 and pPM-h1. Sequence 411 BP; 95 A; 114 C; 92 G; 110 T;	<pre>Query Match 100.0%; Score 411; DB 5; Length 411; Best Local Similarity 100.0%; Pred. No. 8.03e-269; Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre>	1 atgagagtgctgattcttttgtggctgttcacagcctttcctggtatcctgtctgatgt 60	61 cagettcaggagtcgggacctgtcctggtgaagcettctcagtctctgtccctcacctgc 120	121 actgractggctactcaatcaccagtgatcatgcctggagctggatccggcagtttcca 180	181 ggaaacaaactggagtggatgggtacataagttacagtggtatcactaccaaccca 240 	241 tctctcaaaagtcgaatctctatcactcgagacacatccaagaaccagttcttcctacag 300 	301 ttgaattetgtgaetaetggggaeaegteeaeatattaetgtgeaagateeetagetegg 360 	361 actacggctatggactactggggtcaaggaacctcagtcaccgtctcctca 411 	RESULT 2 AC 040462 standard; DNA; 720 BP. AC 040462; DT 20-AUG-1993 (first entry) DE FV(TU27). KW pFV(TU27)-DE; pFV(TU25)-DE; V region; antibody; binding; KW heavy; beta; chain; interleukin; IL-2; receptor; inhibition; KW autoimmune disease; leukemia; cyclosporin; ss. S Home sapiens. No spiens.		MPI 93-145163/18. P-PSDB, R30-145163/18. Balmootide(a) which kind U aboin at human II.2 monanteness.	I Polypeptide(8) Which bind H chain of human 1L-2 receptors - for T treating inflammatory, allergic and auto-immune disorders.
F F S S S S S S S S S S S S S S S S S S	ō m ž	පු දු	do yo	g Vy	යි යි	g &	g &	90 Y2	RESC ID DT DT CKW KW K	PD PR PA	a a a	PT PT

2; 68 AGGACTCGCGCACTCTCTCGTGAACCCTTCTCAGTCTCTGTCCCTCACCTCGACTGTCA 127 ctggctacccaatcaccagtgattatgcctgggactggatccggcagtttccaggaaaca 499 CEGCTACTCAATCACCACTGATCATGCCTGGAGCTGGATCCGGCAGTTTCCAGGAAACA 187 ctgtgactactgaggacacagccacatattactgtgcaagagg--tggtttcccctatg- 676 380 aggagtetggacetggectggtgaaacetteteagtetetgteceteacetgeaetgtea 439 leukaemias etc.
Claim 6; Page 20; 27pp; English.

The constructed plasmids pFv(TU27)-DE and pFv(TU25)-DE which express polypeptides consisting only of the V regions were purified and sequenced. The polypeptides are capable of binding to the beta chain of IL-2 receptor and of inhibiting the binding of IL-2 to the receptor. They are useful as immunomodulators and Gaps immunosuppressants, e.g. to prevent graft rejection or to treat inflammatory allergic and autoimmune diseases, or leukemia. Unlike cyclosporin etc. they are both effective and safe.
Sequence 720 BP; 186 A; 188 C; 170 G; 176 T; Sequence of the anti-urokinase antibody kappa variable region (VK) 0; Mismatches 29; Indels 3; Chimeric monoclonal antibody; anti-urokinase antibody; PCR; antithrombotic agent; myocardial infarction therapy; ss. Query Match 64.5%; Score 265; DB 7; Length 720; Best Local Similarity 90.7%; Pred. No. 1.36e-164; Location/Qualifiers Q25667 standard; cDNA; 378 BP. Matches 312; Conservative (first entry) 10..378 Mus musculus. Key sig_peptide /*tag= a mat_peptide /*tag= b 28-DEC-1992 620 308 440 128 500 188 119 368 g Db ПЪ වු ð δ 윤 δ g õ δ ò

/label= 5'VH1 primer

/*tag= e /label= 3'mVH primer

18..32

misc feature

/*tag= d

/*tag= c /label= VH01 primer misc_feature

1..27

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FI	misc_feature 356371	PN
F.	/*tag= f //abel= 1401 rejmor	PD PD
I N		PR R
PD C	24-JUN-1992.	P.A
7 K	1/-DEC-1991; 121391; 18-DEC-1990; JP-413829.	PA
PR	11-NOV-1991; JP-294464.	DR
PA) TAKEDA CHEM IND LTD.	PT
7 E	Iwasa S, Taka H, Watanabe T, Tada H; Wpt. 02_20652/76	7 5
i ii	1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1	Sa
ΡŢ	Chimeric monoclonal antibodies - contain anti-human fibrin	္ပ
PT	antibody light and heavy chain variable and constant for treating	8
P.T.	thrombolic conditions e.g. myocardial infarction	ខ
<u>ი</u> ც	Example; rigure 13; 0/pp; Engilsh: Polv(A)+ RNA was preod, from mouse anti-urokinase	3 8
ខ	antibody-producing hybridoma UK1-3 cells. Using this poly(A) RNA as	ខ
ខ្ល	a template, an anti-urokinase antibody VK cDNA was amplified with	ខ
8 8	the mC-kappa primer as primer for first strand sysuthesis, and the	ខ្ល
3 8	o my-kappa and o my-kappa pilmers as pilmers for the rok, the amplified fragment was restriction digested and ligated into a	3 8
ខ	restriction fragment of pTB1423 to give an anti-urokinase antibody	t
ဗ္ဗ	WK cDNA contg. plasmid pTB1456. The sequence of this plasmid is	8
S S	given in Q25667. The cDNA is a functional VK gene. The sequence of the primer (MC-gamma-1) is given in 025689.	e ¥
3 8		120
¢,		qq
ō,	Query Match 62.3%; Score 256; DB 4; Length 378;	•
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•	ממוס ויי מייים וייים מייים	qq
g	9 tgaggtgcaactagtggagtcgggacctggcctggtgaaaccttctcagtctctgtccct 68	•
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\$	1,000 10 10 10 10 10 10 10 10 10 10 10 10	Д
og O	69 cactigcactgicactggctactcaatcaccagigatiatgcctggaactggatccggca 128	ć
3		à
7		අු
සු	129 gtttccaggaaacaaactggagtggatgggctacataaactacagtggtaccactagtta 188	ē
δ	174 GTTTCCAGGAAACAAACTGGACGGATGGCCTACATAAGTTACAGTGCTATCACTACCAA 233	Ś
ž		ηρ
2	189 Caacccatctctcaaaagtcgaatctctatcactcgagacacatccaataaccagttctt 748	ò
δ	234 CAACCCAICTCTCAAAAGTCGAATCTCTATCACTCGAGACACACTCCAAGAACCAGTTCTT 293	ÿ
Op	249 cctgcagttgaattctgtgacttctgaggacactgccacatattactgtgcaagat 304	RESU
ó		g p
?		Id
RESI	RESULT 4	Z Z
1 Y	Q67358 standard; DNA; 714 BP. O67358:	M SO
Ħ	27-WAR-1995 (first entry)	FH
음 2	Anti-traseolide 02/01/01 scFv. Rinding protein: immohilization: chimeric protein:	F E
Ž	anchoring protein; Saccharomyces cerevisiae; pUR4143;	N.
ž ž	musk Iragrance; traseclide; polymerase chain reaction; PCR; amplification; primer; light chain; hybridoma; scPv;	PD PF
₹	single chain antibody; monoclonal antibody; ds.	PR :
SO	Synthetic.	PA

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ñ 162 219279 240 339 300 397 43 atgatggtgttaagtcttctgtacctgttgacagcccttccgggtatcctgtcagaggtg 102 61 CAGCTICAGGAGTCGGGACCTGTCCTGGTGAAGCCTTCTCCAGTCTCTGTCCCTCACCTGC 120 9 combination of the two gene segments coding for the variable regions of the antigen binding peptide. The complete sequence of the anti-DNP scFv gene is given in Q66698. Gaps Antibody B is produced as described in EP-141079 and binds to cells They are useful in tumour diagnosis and therapy. See also 206215 for VK of MAb B, 207312-13 for MAb A and 206227-30 TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTCCTACAG ttgaattctgtgactactgaggacacagcacatattactgtgcaagatatggtggta--1 ATCACAGTGCTGATTCTTTTGTGGCTGTTCACAGCCTTTCCTGGTATCCTGTCTGATGTG cagetteaggagteaggacetageetegtgaaacettetetgaetetgteeetegt 163 tetgteactggegaeteeateaceagtggtta---etggaactggateeggaaatteeea gggattaaacttgagtacatgggggtacataagctacagtggtagcacttactacaatcca teteteaaaagtegaateteeateaetegagacaeateeaagaaceagtaetaeetgeag ė Monoclonal antibodies to tumour associated antigens - used for actatg-ctatggagtactggggtcaaggaacctcagtcaccgtctcctca 447 gastrointestinal carcinoma; ovary; pulmonary adenocarcinoma; site of pBluescript. DNA sequencing confirmed the successful DB 11; Length 836; VH domain of antibody B against tumour-associated antigens. almost all gastrointestinal carcinomas and to certain ovary Ë 0; Mismatches 58; Indels 207 Tumour-associated antiqen; murine monoclonal antibody B; 213 G; Pred. No. 4.39e-156; carcinomas and pulmonary adenocarcinomas 61.6%; Score 253; 198 C; diagnosis of malignant tumours etc. HH? Disclosure; Page 12; 18pp; German. Seemann G, Sedlacek 218 A; BP. Best Local Similarity 84.4%; = 22-JAN-1991 (first entry) Matches 347; Conservative Q06214 standard; DNA; 351 (BEHW) BEHRINGWERKE AG. Bosslet K, Seemann G, Se 21-MAR-1990; 105322. 24-MAR-1989; DE-909799. WPI; 90-291873/39. 836 BP; P-PSDB; R07318. diagnosis; ss. Mus musculus. 26-SEP-1990. EP-388914-A. Sequence Query Match 006214; 103 220 181 280 241 340 301 398 361 RESULT ID Q0 g 888888 g 셤 g g 요 à 염 ð à ð à δ Š

Sequence

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? 182 237 242 299 357 103 gtgaaactgctcgagtcaggacctggcctcgtgaaaccttctcagtctctgtctctcacc 162 CCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTCCTA 297 Gaps Clone 2b is one of the plaques which reacted with NPN. The sequence of E. coli for the assemby of heterodimeric Fab molecules. The DNA homologues were prepd. and inserted into a DNA expression vector. of clone 2b Fd chain is given in Q30706. The sequence of the kappa ccaggaaacaaactggaatggatgggctacataagctacgacggtgtcaataagtatgat In the example, the inventors constructed dicistronic vectors for expressing the heavy (Fd consisting of VH and CH1) and light (Kappa) chains (VL,CL) of antibodies targeted to the periplasm 63 tgctctgtcactgactactccatcaccagtgcttattactggaactggatccggcagttt 243 aagttgatttctgtgacttctgaggacacaggaacatatgactgttcaagaggg--a-ct VH and VL DNA homologues were then randomly combined on the same expression vector, Anti-nitrophenylphosphonamidate (NPN) reactive light chain variable and constant regions are given in Q30707 and Sequence of Clone 21b expressing variable heavy (VH) and constant antibody, in its coat protein, useful for diagnostic assay, also new phage DNA libraries and mutagenic oligo:nucleotide primers 3 heterodimer-producing dicistronic vectors were then selected Filamentous phage expressing hetero:dimeric receptor - esp. 190 T; ch 51.8%; Score 213; DB 5; Length 798; 1 Similarity 82.2%; Pred. No. 8.10e-128; 291; Conservative 0; Mismatches 60; Indels Nitrophenylphosphonamidate; NPN; ligand; receptor binding; 179 G; immunoglobulin; light chain; heavy chain; ss. 239 C; Example; Page 188; 229pp; English. 셤

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Db 283 ccatctctcaagaatcgaatctccatcactcgtgacacatctaacaatcagttttccag 342		Db 343 aagttgatttctgtgacttctgaggacacaggaacatatgactgttcaagagga-ct 399	Db 400 agggeetetgetatggaetactggggteaaggaattteagteacegteteetea 453	Qy 358 cGaCTACGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACGTCTCCTCA 411	RESULT 11 ID 031365 standard; DNA; 438 BP. AC 021365;	pUC-RVh-PM1f- Human; antibo complemantari		/ tag= a sig_peptide /*tag= b	FT mat_peptide 69425 FT /*tag= c PN W09219759-A.		PR 19-FEB-1992; JP-032084. PA (CHUS) CHUGAI SEIYAKU KK. DI Bondia MM Jones ET SCIldaha TW Scholk Franchius M.		FI determining regions PS Disclosure, Page 142-3; 207pp; Japanese. CC The sequences given in 231360-6 and Q31355-66 are plasmids encoding CC protitions of monoclanal antichodisc which was daried from monoc	CC (CDR's) was isolated by polymerase chain reaction. The antibodies		CC the hybridoma cells. SQ Sequence 438 BP; 105 A; 123 C; 113 G; 97 T;	Query Match 40.6%; Score 167; DB 5; Length 438; Best Local Similarity 72.6%; Pred. No. 1.45e-95; Matches 288; Conservative 0; Mismatches 101; Indels 0; Gaps 0;	Db 57 ggtgtccactcccaggtccaactgcaggagagggggccaggtctgtgggacctagccag 116	Db 117 acctgagctgacctgcaccgtgtctggctactcaattaccagcgatcatgcctggagc 176
Qy 58 GTGCAGCTTCAGGAGTCGGGAACCTTCTCAGTCTTCTGTCCTCTCTCT	Db 163 tgctctgtcactgactactccatcaccagtgcttattactggaactggatccggcagtt 22	Qy 118 TGCACTGTCACTGGGTACTCAATCACGAGTGATGATGGCTGGAGGTGGAGGTTT 177 Db 223 ccaggaaacaaactggaatggatgggctacataagctacgacggtgtccaataagtatgat 282		Db 283 ccatctctcaagaatcgaatctccatcactcqtgacacatctaacaatcagttttccag 342 	Db 343 aaqttgatttctgtgacttctgaggacacaggaacatatgactgttcaagaggga-ct 399 	400 agggeototgetatggactactggggtcaaggaattcagtcaccgtctcctca 453	SULT 10	V=====================================	DE Fd phage clone sequence comprising kappa light chain regions. KW Expression; kappa light chain; antibody; expression vector; KW bacteriophage; clone; Fd; ds.	OS Synthetic. PN W09405781-A. PD 17-MAR-1994.			FI ingulation a sample PS Example 2f; Page 198; 232pp; English. CC This synthetic sequence was packaged into the filamentous phage Fd. CC Tt commercase than a light chain way and constant rations. The	clone encodes anti-NPN (Nitrophenylphosphonamidate) reactive heterodimers.	Sequence 798 BP; 190 A; userv Match 51.8%;	Similarity 82.2%; Pred. No. 8.10e-128 91; Conservative 0; Mismatches 60	Db 103 gtgaaactgctcgagtcaggactcgtgaaaccttctcagtctctgtctctcac 162 	Db 163 tgctctgtcactgactactccatcaccagtgcttattactggaactggatccggcagttt 222 	Db 223 ccaggaaacaaactggaatggatggctacataagctacgacggtgtcaataagtattat 282

US-08-137-117B-30.mg

;**`** MAb; envelope; glycoprotein; gp120; HIV; AIDS; doma; polymerase chain reaction; PCR; heavy; light; ne deficiency; ss. tgcaccgtgtctggctactcaattaccagcgatcatgcctggagc 254 ocatototoaaatocaqaqtgacaatgotgaqagacaccagoaag 374 agactcagcagcgtgacagccgccgacaccgcggtttattattgt 434 oggactacggctatggactactggggtcaaggcagctcgtcaca 494 recognises human interleukin-6 receptor (II-6R). The cells were transformed with plasmids containing fragments tibody gene which caused the production of the antibody from Gaps ; 0 172 T; 40.1%; Score 165; DB 5; Length 706; 72.4%; Pred. No. 3.59e-94; ative 0; Mismatches 102; Indels 183 6; 177 C; 174 A; , 351 BP. entry)

Location/Qualifiers 141 A; Q42699 standard; DNA; 348 BP 01-NOV-1993 (first entry) (NISB) JAPAN TOBACCO INC. Honjo T, Matsuda F; WPI; 95-006791/01. P-PSDB; R66320 Homo sapiens. 10-MAY-1993; sig_peptide /*tag= a ga 583 II GA 348 Sequence 042699; VH411. Jul 8 08 52 462 582 347 qq g δ 엄 8 염 ð g Š 염 δ ð 9 ö represents a naturally occurring polyreactive antibody which binds to many antigens. Ab26 shares greatest sequence similarity with germline 110 tgtccctcacttgcactgtctctggtggctccatcagtagtggtgattactggagctgga 169 170 tecgecageacecagggaaggggetggagtggattgggtacatatattacagtgggagea 229 167 TCCGGCAGTTTCCAGGAAACAAACTGGAGTGGATGGGCTACATAAGTTACAGTGGTATCA 226 230 ccaactacaacccctccaagagtcgagttgccatatcagtggacacgtctaagaacc 289 50 tectgteceaggtgeagetgeaggagtegggeeeaggaetggtgaageetteaeagaeee 109 47 rccrgrcrargrccagcrrcaggagrcggaccrgrcagrgaagccrrcagrcr 106 227 CTACCTACAACCCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACC 286 The nucleotide sequence of rearranged F105 Vh (Q42698) was compared to two monoclonal antibodies (Ab26 - Q42702) and 268-D - Q42703), which by nucleotide sequence analysis, appear to use a rearranged Vh 71-4 gene (Q42697), was derived from CD5+ B cells of a healthy donor and Gaps 290 agttctccctgaagctgagctctgtgaccgctgcggacacggccgtgtattactgtgc 347 Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain; gp120DNA segments encoding monoclonal antibody - which binds to gpl2 and neutralises HIV, for treating AIDS, and for diagnosing and monitoring HIV infection
Disclosure; Page 62-63; 109pp; English. ; 0 Score 162; DB 7; Length 351; 0; Mismatches 68; Indels 81 T; cosmid; placenta; vector; pJB81; E.coli; mammalian; ds Haseltine WA, Marasco WA, Posner MR, Sodroski JG; WPI; 93-214174/26. US-08-137-117B-30.mg /product= human immunoglobulin variable heavy chain /note= "miscellaneous signal, does not conform to Pred. No. 4.41e-92; 66 (NEWE-) NEW ENGLAND DEACONNESS HOSPITAL CORP 66 C; Location/Qualifiers terminator or splice site sequence" Human immunoglobulin Vh gene #28. Q78966 standard; DNA; 624 BP 72 A; Query Match 39.4%; Best Local Similarity 77.2%; 03-AUG-1995 (first entry) 230; Conservative 151..583 584..586 10-MAY-1993; J00603. Sequence 351 BP; P-PSDB; R38669 Homo sapiens. W09426895-A. misc_signal 24-NOV-1994 /*tag= b /*tag= a /*tag= intron

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The fragments were separated by gel elecrophoresis and 35-45 kb fractions were collected. The fragments were ligated with Clal-digested cosmid vector pJB81. The ligation products were in vitro packed and infected into E.coli 490A. The fragments were then subcloned by colony hybridisation. The Vh genes and the DNA fragments encoding them are
                                                                                    Disclosure; Page 67-68; 130pp; Japanese.

A series of genes (Q78939-79002) encoding human immunoglobulin variable heavy chains. The genes were isolated and cloned from a series of cosmic constructs; Y202; Y103; Y21; Y6;Y24; 3-31; M84; M118 and M131, by PCR amplification using primers Q78917-38. The genes are subdivided into 5 families of Vh genes. The fragments cover a region of 800 kb. The DNA fragments were isolated from high molecular weight DNA from human placenta. The DNA was partially digested with TagI restriction enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monoclonal antibody; MAb; envelope; glycoprotein; gpl20; HIV; AIDS; CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167 TCCGGCAGTTTCCAGGAAACAAACTGGAGTGGATGGGCTACATAAGTTACAGTGGTATCA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       227 CTACCTACAACCCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACC 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            287 AGTICTICCIACAGTIGAATICTGIGACTACTGGGGACACGICCACATATIACTGIGCAA 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    282 tectgteccaggtgeagetgeaggagtegggeecaggaetggtgaageetteggaeaeee 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  402 tocggcagccccagggaagggactggagtggattgggtacatctattatagtgggagca 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cctactacaacccgtccctcaagagtcgagtcaccatgtcagtagacacgtccaagaacc 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                522 agttctccctgaagctgagctctgtgaccgccgtggacacggccgtgtattactgtgcga 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 342 tgtccctcacctgcgctgtctctggttactccatcagcagtagtaactggtgggctgga 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA fragment comprising human immunoglobulin Vh genes - for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful in producing human immunoglobulin in mammalian hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 38.9%; Score 160; DB 13; Length 624; Best Local Similarity 76.5%; Pred. No. 1.09e-90; Matches 231; Conservative 0; Mismatches 71; Indels
                                              production of human immunoglobulin in mammalian hosts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      =
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chain; epitope; immune deficiency; ss.
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227 ccaactacaaccctccctcaagagtcgagtcaccatatcagtagacacgtccaagaacc 286 50 tectgteceaggtgeagetgeaggtggagtegggeeeaggaetggtgaageetteggagaeee 109 0; Mismatches 64; Indels 3; Gaps monitoring HIV infection
Disclosure; Page 56-58; 109pp; English.
The nucleotide sequence of rearranged F105 Vh (Q42698) was compared
to several similar germline Vh IV genes. F105 Vh shares greatest
sequence similarity with germline Vh 71-4 (Q42697). Non-rearranged
Vh IV germlines Vh 4.11 (Q42699), 4.15 (Q42100) and 4.16 (G42701),
that were identified by PCR amplification of genomic DNA from an
adult healthy Caucasian donor, are most closely related to Vh 71-4.
Sequence 348 BP; 72 A; 101 C; 97 G; 78 T; 24-UN-1992.
10-DEC-1992; U10928.
10-DEC-1991; US-804652.
(DAND) DANA FARBER CANCER INST INC.
(NEWE-) DANA FARBER CANCER INST INC.
HASSLING WA MARASCO WA, POSNET MR, SOCIOSKI JG;
WPI; 93-214114726.
DNA segments encoding monoclonal antibody - which binds to gpl20 and neutralises HIV, for treating AIDS, and for diagnosing and Query Match 37.2%; Score 153; DB 7; Length 348; Best Local Similarity 77.8%; Pred. No. 7.98e-86; 235; Conservative 205..252 148..162 misc_RNA /*tag= d /label= CDR2 /*tag= c /label= CDR1 mat_peptide /*tag= b ga 348 II GA 348 W09312232-A misc_RNA 347 347 Matches g 셤 ô 셤 ð g à 8 9 ð 임 δ

Search completed: Mon Jul 8 09:03:06 1996 Job time: 42 secs.

128:enEST20 129:enEST21 130:enSTS1 131:enSTS2 132:enSTS3

US-08-137-117B-30 rat

Mean 9.954; Variance 1.799; scale 5.535 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

F213974 Homo sapies 1.01e-239 E2T13874 Homo sapiens 1.08e-164 EST13874 Homo sapiens 1.08e-164 yo59b04.rl Homo sapiens 3.57e-158 EST13381 Homo sapiens 6.72e-141 EST13381 Homo sapiens 6.72e-141 EST30734 Homo sapiens 1.19e-100 EST1398 Homo saptems 4.58e-80 y j68a01.rl Homo saptem 5.50e-68 yc01g07.rl Homo saptems 1.36e-37 EST91759 Homo saptems 1.36e-33 EST89449 Homo saptems 8.53e-32 EST89449 Homo saptems 8.53e-32 S.scrofa mRNA; expres 5.15e-30 ys11b01.r1 Homo sapie 2.99e-28
yo70q05.r1 Homo sapie 8.91e-25
yo70q05.r1 Homo sapie 8.91e-25
yo70q05.r1 Homo sapie 1.02e-19
yj75f04.r1 Homo sapie 1.02e-19
yj75f04.r1 Homo sapie 1.02e-19
yj163.r1 Homo sapie 1.83e-16
yp13a12.r1 Homo sapie 8.57e-12
yb86f08.r1 Homo sapie 8.57e-12
yb86f08.r1 Homo sapie 8.57e-12
yb86f08.r1 Homo sapie 8.57e-12
yb65f02.r1 Homo sapie 2.67e-10
yp13a12.r1 Homo sapie 2.67e-10
yp13a12.r1 Homo sapie 2.67e-10
yp13a04.r1 Homo sapie 7.62e-09
yp13b04.r1 Homo sapie 7.62e-09
yp13b04.r1 Homo sapie 7.62e-09
yp15b06.r1 Homo sapie 7.62e-09
yu69e06.r1 Homo sapie 1.99e-07
yu69e06.r1 Homo sapie 1.99e-07 yp21g01.rl Homo sapie 1.01e-239 yp21g01.rl Homo sapie 1.01e-239 EST30734 Homo sapiens 1.19e-100 S.scrofa mRNA; expres 5.15e-30 y140b06.rl Homo sapie 2.99e-28 ys11b01.rl Homo sapie 2.99e-28 ys11b01.rl Homo sapie 2.99e-28 EST13989 Homo sapiens 4.58e-80 7063q08.rl Homo sapie y138e08.rl Homo sapie Human Chromosome 4 (c EST110390 Rattus sp. Description H33938 RS 9382 HS4STS735 HUM4STS735 H22208 T27727 H30111 T27715 H30111 T27715 T28164 H8727130 T48619 T60021 T27730 R48619 T60021 T29661 T29661 C H871610 SSC1010 SSC1010 SSC1010 SSC1010 SSC1010 H2604 H3952 H3962 H3952 H3962 H3952 HS753236 HST27727 ΙD 1127 69 T 447 B 1700 T 127 69 13 13 69 127 127 DB 53 16 10 78 2448 2448 2448 2448 2548 2648 2788 Query Match Length Score

95:9012319 96:90EST2 97:90EST3 98:90EST4 99:90EST5 100:90EST6 101:90EST7 102:90EST8 103:90EST9 104:90EST10 105:90EST11 106:90EST3 112:90EST4 103:90EST4 113:90EST1 110:90EST2 111:90EST3 112:90EST4 113:90EST5 114:90EST6 115:90EST7 116:90EST8 117:90EST9 118:90EST10 119:90EST11 120:90EST2 121:90EST13 122:90EST14 123:90EST15 124:90EST16 125:90EST17 126:90EST18 127:90EST19

EST-STS-TWO

Database:

H43753

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31-JUL-1995

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Release 2 Copyright D	2.1D John F. Collins, Biocomputing Research Unit. t (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.
MPsrch_nn n.a	n.a. database search, using Smith-Waterman algorithm
Š.	n Jul 8 09:03:25 1996; MasPar time 190.43 Seconds 775.895 Million cell updates/sec
מתרחתר זומר	denet aceu.
Title: >U Description: (1. Perfect Score: 41 N.A. Sequence: Comp:	VUS-08-137-117B-30 (1-411) from US08137117B.seq 411 1 ATGAGAGTGCTGATTTTCCTCAGTCACCGTCTCCTCA 411 TACTCTCACGACTAAGAAAAGGAGTCAGGGAGGAGGAG
Scoring table: TABI	TABLE default Gap 6
Nmatch STD : Db	Dbase 0; Query 0
Searched: 51	518261 seqs, 179750453 bases x 2
Post-processing: Mi	Minimum Match 0% Listing first 45 summaries
Database: ES	1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8 9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14 15:EST16 11:EST11 12:EST12 13:EST13 14:EST14 15:EST14 15:EST14 15:EST17 18:EST19 19:EST19 20:EST12 21:EST12 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26 27:EST27 28:EST28 29:EST28 29:EST38 33:EST33 34:EST38 33:EST38 34:EST38 33:EST38 34:EST38 35:EST38 35:EST48 49:EST49 50:EST40 55:EST56 55:EST56 55:EST56 55:EST56 55:EST56 55:EST56 55:EST58 55:
Database: F.S.	T-STS-TWO

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US-08-137-117B-30 m

DEFINITION	ION yp21q01.r1 Homo sapiens cDNA clone 188112 5' similar to qb:123556		
NOT COLLOCK	IG HEAVY CHAIN V-II REGION (HUMAN);	ΩP	193 gccaactae
ACCESSION KEYWORDS	H43/33	Qy	226 ACTACCTAC
SOURCE	human clone=188112 library=Soares breast 3NbHBst vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin	· 43	253 canticted
	resistant) primer=M13RP1 Reitel=Not I Reite2=Eco RI Adult human. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'	δ	286 CAGITCIT
	TGTTACCAATCTGAAGTGGGAGCGCCCCCTTTTTTTTTT		
	digested with Not I and cloned into the Not I and Eco RI sites of a	RES	RESULT 2
	modified pills vector (rhatmacia), Library Well through one found of normalization to a Cot = 20. Library constructed by Bento Soares	AC AC	H43753;
ORGANISM	and M.Fatima Bonaldo.	TO E	17-NOV-1995 (F
	Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;	田田	yp21g01.rl Hor
	Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcootervaii: Choanata: Tetrapoda; Amniota: Mammalia: Theria:	H &	IG HEAVY CHAIN FST.
ackadaaad	Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.	SOS	Homo sapiens
AUTHORS	I (bases I to 476) Hillier, I., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,	38	Eukaryota; An Theria; Euther
	Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,	RP RP	[1] 1-478
	Trevaskis, E., Materston, R., Williamson, A., Wohldmann, P. and	E E	Hillier L., C
TITLE	Wilson, K. The WashU-Merck EST Project	& &	Holman M., Hu. Parsons J., R.
COMMENT	Unpublished (1995)	RA	Trevaskis E.,
	Contact: Wilson RK	RI.	Unpublished.
	WashUnster Injustrity School of Modicina	ខ	Contact: Wilso
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108	38	MO 63108 Tel:
	Tel: 314 286 1800	ខ្ល	est@watson.wu
	rax: 314 266 1610 Frail: eatewatson.wonstl.edu	3 8	Consortium, Li
	High quality sequence stops: 278	88	information.
	Source: image consortium, minu This clone is available rovalty-free through LINE; contact the	E E	key
	IMAGE Consortium (info@image.llnl.gov) for further information.	E	source
FEATURES	NCBI gi: 919805 Location/Oualifiers		
source	1.,478	SS	Sequence 478
	/olganism= nomo sapiens /clone="188112"	α.	Query Match
BASE COUNT	/note="human" 94 a 129 c 137 g 110 t 8 others	∞ Σ	Best Local Simil: Matches 224;
Onerv Mato		d	15 tectgtee
Best Local	Best Local Similarity 75.2%; Pred. No. 1.01e-239; Matches 224; Conservative 0; Mismatches 71; Indels 3; Caps 3;	Qy	47 rccrgrcr
Db 15 to	15 tectqteeeaqqtqeaqetqqaqteqqqqeeeaqqaeteqqtqaaqeetteqqaqaee 74	QQ	75 ctgtccct
11 Qy 47 TC		0y	106 CTGTCCT
	ctgtccctcanctgctcttgttggttggttccatcaataatntac-tac-tggaattgg 132	qq	133 atccggca
Qy 106 CT		Qy	166 ATCCGCCA
Db 133 at	tccggcagtccccagggaagggactggagtggattggctatatctattacagtgggaac 192	ga	133 gccaacta
) Qy 166 AT		ð	226 ACTACCTA

agtccccagggaagggactggagtggattggctatatctattacagtgggaac 192 ccaggigcagcigcaggagiccgaggacicggigaagcciicggagacc 74 ustl.edu High quality sequence stops: 278 Source: IMAGE LINL This clone is available royalty-free through LINL e IMAGE Consortium (info@image.llnl.gov) for further NCBI gi: 919805 Location/Qualifiers Gaps Clark N., Dubuque T., Elliston K., Hawkins M., Iultman M., Kucaba T., Le M., Lennon G., Marra M., Rifkin L., Rohlfing T., Soares M., Tan F., , Waterston R., Williamson A., Wohldmann P., Wilson R.; lerck EST Project"; (Rel. 45, Created) (Rel. 45, Last updated, Version 1) omo sapiens cDNA clone 188112 5' similar to gb:L23556 son RK WashU-Merck EST Project Washington University dicine 4444 Forest Park Parkway, Box 8501, St. Louis, : 314 286 1800 Fax: 314 286 1810 Email: nimalia; Metazoa; Chordata; Vertebrata; Mammalia; eria; Primates; Haplorhini; Catarrhini; Hominidae. 3, Score 137; DB 123; Length 478; Pred. No. 1.01e-239; 0; Mismatches 71; Indels /note="human" BP; 94 A; 129 C; 137 G; 110 T; 8 other; /organism="Homo sapiens"/clone="188112" tandard; RNA; EST; 478 BP. IN V-II REGION (HUMAN); 33.3%; larity 75.2%; Conservative (human)

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g ð RESULT

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US-08-137-117B-30 rat

5 T27727 164; Query Match source COUNT ORGANISM mRNA Matches ACCESSION AUTHORS JOURNAL REFERENCE FEATURES KEYWORDS TITLE COMMENT ORIGIN SOURCE BASE ð 염 ò ä A Bult C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D.,

A Mite O., Sutton G., Blake J.A., Brandon R.C., Chiu M.W.,

R Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D.,

R FitzGerald L.M., FitzHugh W.M., Fitchman J.L., Geophagen N.S.M.,

R Glodek A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle Jr P.S.,

RA Helley J.M., Klinek K.M., Kelley J.C., Liu L.I., Marmaros S.M.,

MARTICK J.M., MORENO-PALANQUES R.F., McDonald L.A., Nguyen D.T.,

RA Pellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L.,

RA Saudek D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R.,

RA Weidman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A.,

R. Coleman T.A., Collins E.J., Dimke D., Feng P., Ferrie A.,

R. Fischer C., Haetings G.A., He W.W., Hu J.S., Greene J.M.,

Gruber J., Hudson P., Kim A., Kosak D.L., Kunsch C., Ji H., Li H.,

M. Hassner P.S., Olsen H., Raymond L., Mei Y.F., Wing J., Xu C.,

X. M. Haselline W.A., Fields C., Frasc C.M., Venter J.C.,

M. Haselline W.A., Fields C., Frasc C.M., Venter J.C.,

M. Haselline W.A., Fields C., Frasc C.M., Venter J.C.,

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M. Haselline W.A., Fields C., Frasc C.M., Venter J.C.,

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M. Haselline W.A., Fields C., Frasc C.M., Venter J.C.,

M. Haselline W.A., Fields C., Frasc C.M., Venter J.C.,

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M. Hasel 71 tectgteccaggtgeagetgeaggagtegggeecaggaetggtgaageetteggagaeee 130 131 tgtccctcacctgcactgtctctggtggctccatcagtagtta-c-tac-tggagctgga 187 107 TGTCCCTCACCTGCACTGTCACTGGCTACTCAATCACCAGTGATCATGCCTGGAGCTGGA 166 188 tecggcagececeagggaagggaetgeagtggattgggtatatgtattaeagtgggagea 247 Indels 3; Gaps 286 CACTICTICCTACACATICATACTCTCACTACTGGGGCACACGTCCACATATACTGTG 343 253 cagttctccctgaagttgacttctgcgaccactgcggacacggccgtctattactgtg 310 and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org). NCBI gi: 609825 Contact: Venter, JC The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878 Tel: 3018699056 Fax: 3018699423 Email: tdbinfo@tdb.tigr.org For clone availability, additional sequence EST13874 Homo sapiens cDNA 5' end similar to immunoglobulin mu (gamma) heavy chain, $V(IV)\,DJC$ regions (HT:3057). Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae Score 103; DB 127; Length 299; Pred. No. 1.08e-164; "Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence"; Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A., BP; 61 A; 84 C; 82 G; 68 T; 4 other; 0; Mismatches 45; v.-orr-1990 (Rel. 45, Last updated, Version 2)
EST13874 Homo sapiens cDNA 5' end similar to 'n /organism="Homo sapiens" JT 3
HST27727 standard; RNA; EST; 299 BP. Location/Qualifiers Created) /note="human" 25.1%; Best Local Similarity 77.4%; 164; Conservative <1..>299 12-JAN-1995 (Rel. 42, 07-SEP-1995 (Rel. 45, Homo sapiens (human) Sequence 299 Unpublished. Query Match source Matches mRNA

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Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.C., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A., Fischer, C., Hastlings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Klim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldher, R.A.,
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Glodek, A., Ghehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr.P.S.,
Kelley, J.M., Klimek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M.,
Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Initial Assessment of Human Gene Diversity and Expression Patterns Email: tdbinfo@tdb.tigr.org For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database ; ; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C. LOCUS T27727 299 bp mRNA EST 06-SEP-1995 DEFINITION EST13874 Homo sapiens cDNa 5' end similar to immunoglobulin mu (gamma) heavy chain, V(IV) DJC regions (HT:3057). 167 TCCGCCACTTTCCACGAAACAAACTGGAGTGGATGGCTACATAACTTACAGTGTATACA 226 Gaps Sutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 3, Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Score 103; DB 69; Length 299; Pred. No. 1.08e-164; 45; Indels 4 others Based Upon 52 Million Basepairs of cDNA Sequence human primer=M13 Reverse library=Human Testis. The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878 0; Mismatches u 89 248 ccgactacaaccentnecteaagagtegagte 279 227 CTACCTACAACCCATCTCTCAAAAGTCGAATC 258 /organism="Homo sapiens" Location/Qualifiers ъ 82 (tdbinfo@tdb.tigr.org). /note="human" 77.48; 25.1%; Contact: Venter, JC 84 c (bases 1 to 299) Conservative Unpublished (1995) <1..>299 1..299NCBI gi: 609825 Tel: 3018699056 Fax: 3018699423 Best Local Similarity Homo sapiens æ

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Mainte, V., Lee, N. Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W., Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzechald, L.M., FitzHugh, W.M., Fitzchman, J.L., Geoghagen, N.S.M., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr.P.S., Kalley, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Uterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A., Fischer, C., Hastings, G.A., Hew, H., J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Fannon, M.R., Rosen, C.A., K., C., V., Fannon, M.R., Rosen, C.A., K., H., M., L., Kneen, C.A., M., M., L., Fannon, M.R., Rosen, C.A., K., M., M., L., Fannon, M.R., Rosen, C.A., K., M., M., Fannon, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C. Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence Unpublished (1995) T27715 331 bp mRNA EST 06-SEP-1995 EST13381 Homo sapiens cDNA 5' end similar to immunoglobulin gamma heavy chain V region (GB:M97921) (HT:3789). ; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; 58 gtgcagctacaggagtcggggcccgggactggtgaagccttcggagaccctgtccctcacc 117 58 GTGCAGCTTCAGGAGTCGGGACCTGTCCTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCC 117 178 tcccccgggaagggcctggagtggattgggactctctattatactgggaagctcgtactac 237 238 aaccegtecetegagagtegagteacettetetettgacaegtecaagaaceaettetee 297 118 TGCACTGTCACTGGCTACTCAATCACCAGTGAT-CATGC--CTGGAGCTGGATCCGGCAG 174 235 AACCCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACCACTCCAAGAACCAGTTCTTC 294 Gaps Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo ä Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Length 410; 298 cttatgctgacctctgtaaccgccgcagacacggctgtatattgtg 346 295 CTACAGTTGAATTCTGTGACTACTGGGGACACGTCCACATATTACTGTG 343 2 others 0; Mismatches 84; Indels human primer=M13 Reverse library=Human Testis. Pred. No. 3.57e-158; Score 100; DB 13; 100 5 /clone="182191" _ = = = /note="human' Query Match 24.3%; Best Local Similarity 69.9%; 131 c (bases 1 to 331) 202; Conservative Homo sapiens ø 67 T27715 EST. ٠ BASE COUNT ORIGIN DEFINITION ORGANISM Matches ACCESSION KEYWORDS SOURCE AUTHORS JOURNAL REFERENCE TITLE RESULT g 셤 염 g g ð 8 ð ð δ

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KEYWORDS 음 g 염 g g à ð δ δ ð information related to this EST, please contact the TIGR Database ; 132 tgtccctcacttgcactgtctctggtgtntccgtctacagtgacaattttnactggggct 191 192 gggtccgccaggccccaggaaaggggctggagtggattgggactattttnatagtggga 251 164 GGATCCGGCAGTTTCCAGGAAACAAACTGGAGTGGGTTGGGCTACATAAGTTACAGTGGTA 223 252 caacctactacaaccngtccctcaggagtcgagtcaccatttccgtngacangtccagaa 311 224 TCACTACCACCCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGA 283 72 tectyteccayetycayetycaygayteyyyeecayyaetyytyaayeetteyyayaeee 131 Gaps Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A., Bult C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D., White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.W., Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., FirzGerald L.M., FirzHugh W.M., Fritchman J.L., Geoghagen N.S.M., Glodek A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle Jr P.S., Kelley J.M., Klimek K.M., Kelley J.C., Liu L.I., Marmaros S.M., Email: tdbinfo@tdb.tigr.org For clone availability, additional sequence and expression 12-JAN-1995 (Rel. 42, Created) 07-SEP-1995 (Rel. 45, Last updated, Version 2) EST13381 Homo sapiens cDNa 5' end similar to immunoglobulin gamma heavy chain V region (GB:M97921) (HT:3789). ć, Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Length 331; 8 others 0; Mismatches 73; Indels Score 92; DB 69; Lk Pred. No. 6.72e-141; The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878 8 /organism="Homo sapiens" HST27715 standard; RNA; EST; 331 BP Location/Qualifiers б 16 (tdbinfo@tdb.tigr.org). /note="human" Query Match 22.4%; Best Local Similarity 70.0%; 90 c 177; Conservative <1..>331 Contact: Venter, 1..331 NCBI gi: 609813 284 ACCAGTTCTTCCT 296 Tel: 3018699056 Fax: 3018699423 312 acaagttctccct 324 Homo sapiens (human) æ 62 source 1-331 Matches BASE COUNT ESA A FEATURES ORIGIN 셤 요 g à 유 5 윤 à ð

2; T28164 234 bp mRNA EST 06-SEP-1995 EST30734 Homo sapiens cDNA 5' end similar to immunoglobulin heavy Deuterostomia, Chordata, Vertebrata, Gnathostomata, Osteichthyes, Sarcopterygii, Choanata, Tetrapoda, Amniota, Mammalia, Theria, Eutheria, Archonta, Primates, Catarrhini, Hominidae, Homo. A Merrick J.W., MORENO-PALANQUES R.F., McDonald L.A., Nguyen D.T.,
A Sandek D.M., Shirley R., Small K.V., Spridgs T.A., Utterback T.R.,
A Meidman D.T., Li Y., Bedral D.P., Cap L., Cepeda M.A.,
A Coleman T.A., Collins E.J., Dimke D., Feng P., Ferrie A.,
Eischer C., Hastings G.A., He W.W., Hu J.S., Greene J.M.,
A Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li H.,
A Meissener P.S., Olsen H., Raymond L., Wei Y.F., Wing J., Xu C.,
A Yu G.L., Ruben S.W., Dillon P.J., Fannon M.R., Rosen C.A.,
A Haseltine W.A., Fields C., Fraser C.M., Venter J.C.; 251 252 caacctactacaaccngtccctcaggagtcgagtcaccatttccgtngacangtccagaa 311 72 tectgteceagetgeagetgeaggagtegggeeeaggaetggtgaageetteggagaeee 131 132 tgtccctcacttgcactgtctctggtgtntccgtctacagtgacaattttnactggggct 191 107 TGTCCCTCACCTGCACTGTCACTGGCTACTCAATCACCAGTGATCATG--C-CTGGAGCT 163 164 GGAICCGGCAGTITCCAGGAACAAACTGGAGTGGATGGGCTACATAAGTIACAGTGGTA 223 Gaps Contact: Venter, JC The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878 Tel: 3018699056 Fax: 3018699423 Email: thabinfoldab.tigr.org For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfoldab.tigr.org). NCBI gi: 609813 H., 192 gggtccgccaggccccaggaaaggggctggagtggattgggactattttnatagtggga 3; Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; "Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence"; Length 331; Score 92; DB 127; Length 33: Pred, No. 6.72e-141; 0; Mismatches 73; Indels human primer=M13 Reverse library=Human Colon. BP; 62 A; 90 C; 91 G; 80 T; 8 other; chain V, D, J regions (GB:Z14206) (HT:3118) /organism="Homo sapiens" Location/Qualifiers /note="human" Query Match 22.4%; Best Local Similarity 70.0%; Matches 177; Conservative 1 (bases 1 to 234) ..>331 11 ||||||| 111 284 ACCAGTTCTTCCT 296 312 acaagttctccct 324 Homo sapiens T28164 Sequence 331 Unpublished. œ SOURCE ORGANISM source DEFINITION mRNA REFERENCE ACCESSION

Homo sapiens (human) T27730; source 132 mRNA RESULT KE BE BE 염 ð a 임 à A ð Merrick J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pellogrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Meidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C. Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldher, R.A., Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr.P.S., Kelley, J.M., Klimek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Initial Assessment of Human Gene Diversity and Expression Patterns Email: tdbinfo@tdb.tigr.org For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database ö 47 ICCIGICIGAIGIGCAGCIICAGGAGICGGGACCIGICGIGGIGAAGCCIICICAGICIC 106 132 tgtccctcacctgngctgtctctggttactccataagaagtggttactactggggctgga 191 Gaps 12-JAN-1995 (Rel. 42, Created) 07-SEP-1995 (Rel. 45, Last updated, Version 2) EST30734 Homo sapiens CDNA 5' end similar to immunoglobulin heavy ö Length 234; 0; Mismatches 36; Indels 6 others Based Upon 52 Million Basepairs of cDNA Sequence Pred. No. 1.19e-100; Score 73; DB 69; The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878 chain V, D, J regions (GB:Z14206) (HT:3118). 25 /organism="Homo sapiens" В. Location/Qualifiers 72 g HST28164 standard; RNA; EST; 234 T28164; (tdbinfo@tdb.tigr.org). 192 ttcggcanggcccagggaac 211 167 TCCGCCAGTTTCCAGGAAC 186 /note="human" 17.8%; Best Local Similarity 74.3%; Contact: Venter, JC 63 G 104; Conservative Unpublished (1995) <1..>234 ...234 Tel: 3018699056 NCBI gi: 610262 Fax: 3018699423 ๗ 41 Query Match source BASE COUNT Matches AUTHORS JOURNAL FEATURES TITLE ORIGIN RESULT E E E E E E 셤 유 ð ð ð

Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldher R.A.,
Bult C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D.,
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A Weidman J.F., Li Y., Bedrarik D.P., Gao L., Cepeda M.A.,
A Coleman T.A., Collins E.J., Dinke D., Feng P., Ferrie A.,
A Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li H.,
M. Weisener P.S., Olsen H., Raymond L., Wei Y.F., Wing J., Xu C., 72 tectgteccaggtgeagetgeaggtegggneeaggnetggtgaegttttnggagaeee 131 47 TCCTGTCTGATGTGCAGCTTCAGGAGTCGGGACCTGTCTGGTGAAGCCTTCTCAGTCTC 106 tgtccctcacctgngctgtctctggttactccataagaagtggttactactgggggctgga 191 Gaps Contact: Venter, JC The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878 Tel: 3018699056 Fax: 3018699423 Email: chábinGetdeb.tigr.org For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfoetdb.tigr.org). NCBI qi: 610262 12-JAN-1995 (Rel. 42, Created) 07-SEP-1995 (Rel. 45, Last updated, Version 2) EST13989 Homo sapiens cDNA 5' end similar to immunoglobulin heavy 0; Mismatches 36; Indels 0; Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae Patterns Based Upon 52 Million Basepairs of cDNA Sequence"; Unpublished. Query Match 17.8%; Score 73; DB 127; Length 234; Best Local Similarity 74.3%; Pred. No. 1.19e-100; "Initial Assessment of Human Gene Diversity and Expression Yu G.L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A., Haseltine W.A., Fields C., Fraser C.M., Venter J.C.; Sequence 234 BP; 41 A; 63 C; 72 G; 52 T; 6 other; /organism="Homo sapiens" ₩. chain, V region (GB:Z12364) (HT:3115). Location/Qualifiers JT 10 HST27730 standard; RNA; EST; 180 192 ttcggcanggcccagggaac 211 167 TCCGGCAGTTTCCAGGAAAC 186 /note="human" Matches 104; Conservative

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Kelley, J.M., Klimek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J., Dimke, D. Feng, P., Ferrie, A., Fischer, C., Hastings, G.A., He, M.-W., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., 1 (bases I to 180)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.C., Gocayne, J.D.,
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Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr, P.S., Initial Assessment of Human Gene Diversity and Expression Patterns information related to this EST, please contact the TIGR Database DEFINITION yj68a01.rl Homo sapiens cDNA clone 153864 5' similar to gb:L23556 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., genetgtetetggtggetecateageagtggtggttactectggagetggateeggeage 120 Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; TGCAGCTTCAGGAGTCGGGACCTGTCGTGAAGCCTTCTCAGTCTCTGTCCCTCACCT 118 1 tncagctgcaggagtccggctcaggactggtgaagccttcanagaccctgtccctcacct For clone availability, additional sequence and expression Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo 121 caccagggaaagggcctggnagtggattggntacatctatcatagtgggagcac 174 176 TTCCAGGAAACAAAC-TGG-AGTGGATGGCCTACATAAGTTACAGTGGTACATAAC 227 Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C. Length 180; 5 others 0; Mismatches 40; Indels Based Upon 52 Million Basepairs of cDNA Sequence Pred. No. 4.58e-80; Score 63; DB 69; 20878 ų 39 The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 21 /organism="Homo sapiens" Location/Qualifiers ъ Email: tdbinfo@tdb.tigr.org 54 (tdbinfo@tdb.tigr.org) /note="human" 169 bp 15,3%; Best Local Similarity 74.1%; Contact: Venter, JC 49 c 129; Conservative Unpublished (1995) <1..>180 1..180 609828 Tel: 3018699056 Fax: 3018699423 ø NCBI gi: 33 R48619 Query Match 12 source BASE COUNT Matches 59 13 JOURNAL, REFERENCE AUTHORS FEATURES TITLE ORIGIN RESULT LOCUS 염 ð 셤 ð 셤 ð ä EST13989 Homo sapiens cDNA 5' end similar to immunoglobulin heavy Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A.,
Bult C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D.,
A White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.M.,
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A. Merlick J.M., NORRO-PALANQUES R.F., McDonald L.A., Nguyen D.T.,
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Meissner P.S., Olsen H., Raymond L., Wei Y.F., Wing J., Xu C.,
A. Yu G.L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A.,
A. Yu G.L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A., 61 genetytetetggtggetecateageagtggtggttaetectggagetggateeggeage 120 119 GCACTGTCACTGGCTACTCAATCACCAGTGATCATG---CCTGGAGCTGGATCCGGCAGT 175 1 theagetgeaggagteeggeteaggactggtgaageetteanagaceetgteeeteacet 60 06-SEP-1995 Gaps Rd, Gaithersburg, MD 20878 Tel: 3018699056 Fax: 3018699423 Email: tdbinfo@tdb.tigr.org For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org). NCBI gi: 609828 Contact: Venter, JC The Institute for Genomic Research 932 Clopper 121 caccagggaaaggggcctggnagtggattggntacatctatcatagtgggagcac 174 5 Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Haseltine W.A., Fields C., Fraser C.M., Venter J.C., "Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence"; Score 63; DB 127; Length 180; Indels human primer=M13 Reverse library=Human Testis. 33 A; 49 C; 54 G; 39 T; 5 other; 0; Mismatches 40; Pred. No. 4.58e-80; chain, V region (GB:Z12364) (HT:3115) T27730 /organism="Homo sapiens" /note="human" **IIRNA** Location/Qualifiers 180 bp 15.3%; Best Local Similarity 74.1%; 129; Conservative ..>180 Homo sapiens (human) Homo sapiens

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mRNA

source

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Sequence 180 BP;

Query Match

Matches

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ORGANISM

ACCESSION KEYWORDS

RESULT 11 DEFINITION

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Gaps

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ORGANISM

REFERENCE AUTHORS

ACCESSION KEYWORDS

SOURCE

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US-08-137-117B-30 rst

1010	IG HEAVY CHAIN V-II REGION (HUMAN);	rocas	T60021 367 bp mRNA EST 09-FEB-1995
RDS	K48619 EST	DEFINITION	yc01g0/.rl Homo sapiens cDNA clone 79452 5' similar to qb:L23556 IG HEAVY CHAIN V-II REGION (HIMAN);
Ŀ	human clone=153864 library=Soares breast 2NbHBst vector=p7773D	ACCESSION	T60021
	(Pharmacia) with a modified polylinker host=DH10B (ampicillin	KEYWORDS	EST.
	resistant) primer=MI3RP1 Rsite1=Not I Rsite2=Eco RI Adult female.	SOURCE	human clone=79452 library=Stratagene lung (#937210)
	TGTTACCARTCTGAAGTGGGAGCGCCCCCTTTTTTTTTTT		vector-parumescript on- most-sour cerrs (kamamycrn resistant) primer=M13RP1 Rsite1=EcoR1 Rsite2=XhoI Normal lung tissue from a 72
	double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),		year old male. Cloned unidirectionally. Primer: Oligo dT. Average
	digested with Not I and cloned into the Not I and Eco RI sites of a		insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:
	modified pT/T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 230. Library constructed by Rento		5'-GAATTICGGCACGAG-3'; 3' adaptor sequence: 5'-CTCCACTTTTTTTTTTT-3'
	Soares and M.Fatima Bonaldo.	ORGANISM	Homo sapiens
ANISM	Homo sapiens		Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
	Eukaryotae, Metazoa, Eumetazoa, Bilateria, Coelomata, Pontozontomia, Chordata, Wortshorta, Coethoatomata, Octolokhusa,	domadadad	Eutheria; Primates; Catarrhini; Hominidae; Homo.
	Deuteroscomia, choruata, Verceptata, Gharinoscomata, Oscelentinges; Sarcoptervoii: Choanata: Tetrapoda: Amniota: Mammalia: Theria:	ATTHORS	I (Dases I to 367) Billiar I. Clark N. Dubuma T. Elliston K. Hawkins M.
	Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.	caouton o	niillei, i., . claik, n., . bubuque, i., . biliscon, n., . nawains, n., Holman, M., . Hultman, M., . Kucaba, T., . Le, M., . Lennon, G., . Marra, M.,
ENCE	1 (bases 1 to 169)		Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E.,
HORS	Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,	Ē	Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
	hotman,m., hutcman,m., nucaba,i., le,m., lennon,e., marra,m., Paraona J., Riftin I., Rohlfing T., Spares M., Tan R	TITLE	WashU-Merck EST Project
	Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and	COMMENT	original (1999)
-	Wilson, R.		Contact: Wilson RK
RNAL	Ine Washu-werck EJT Project Unpublished (1995)		wasnu-merck EST Project Washington University School of Medicine
IN.			4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
	Contact: Wilson RK		Tel: 314 286 1800
	Mashu-Merck EST Project Washington Injustrativ School of Medicina		Fax: 314 286 1810
	Masilington University School of medicine 4444 Forest Park Parkwav, Box 8501, St. Louis, MO 63108		Email: estewatson.wustl.edu High gality seguence stops: 243
			Source: IMAGE Consortium, LINL
	Fax: 314 286 1810		This clone is available royalty-free through LLNL; contact the
	Email: est@watson.wustl.edu		IMAGE Consortium (info@image.llnl.gov) for further information.
	High quality sequence starts: 1		
	High quality sequence stops: 1	SEATIBES	NCB1 g1: 661838
	Journe: Irange consolicitum, manu This clone is available rovalty-free through LIM. : contact the	REGIONES	nocacion/Quailiteis 1 367
	IMAGE Consortium (info@image.llnl.gov) for further information,	201500	/organism="Homo sapiens"
	Trace considered overall poor quality.		/clone="19452"
	NCBI qi: 810645	BASE COUNT	/note="human" 71 a 112 c 94 a 84 t 6 others
RES	Location/Qualifiers	ORIGIN	
source			
	/organism="Homo sapiens" /clone="153864"	Query Match Best Local	Query Match 10.0%; Score 41; DB 78; Length 367; Best Local Similarity 76.6%: Pred. No. 3.12e-37;
	/note="human"	Matches	ative
COUNT	26 a 56 c 47 g 40 t	Db 1 ac	acot coasgagosant of coot gasact gagot of or gasogosgagasangong 60
;			
ory Match	13.9%; Score 57; DB 47; Length 169; the local etmilarity 78 8%; Drad No 5 50a-60;	Qy 272 A(272 acrcatccargarccagticticctacagtigaatictgigactactggggacacgtcca 331
ches	rvative	Db 61 ta	tattactgtgcgaga 77
į			
35 t	35 toctytoccagottgoagottgoaggattcgggoccaggactgytgaagocttcggagaccc 94 	Qy 332 CI	332 CATATTACTGGGAAGA 348
:	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	RESULT 14	
95 t	95 tgt.ccctcaattgcactgt.ctggtggct.ccatcagca 133 	E	T29716 325 bp mRNA EST 06-SEP-1995 ESTPJ159 Howe sapiens CDNA 5' end similar to immunoglobulin heavy
		ACCESSION	CHAIL ',',', regions (65:8354029) (81:3702). From
JT 13		SOURCE	Esi. human primer=M13 Reverse library=Human Synovial membrane.

TITLE JOURNAL

COMMENT

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RESULT

BASE COUNT

ORIGIN

Query Match 13.9%; Best Local Similarity 78.8%;

Matches

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FEATURES

US-08-137-117B-30 rst

103 rcrcrgrccrcaccrg 119 Unpublished source mRNA 88 148 Matches 43 쇰 쇰 ð 8 Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence Email: tdbinfoëtdb.tigr.org For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; 88 ggtgtcctgtcacaattacagctgcagcagtcaggtccaggactggtgaagccctcgcag 147 43 GGTATCCTGTCTGATGTGCAGCTTCAGGAGTCGGGACCTGTCCTGGTGAAGCCTTCTCAG 102 Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. ö Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C. Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; 0; Mismatches 19; Indels Query Match 9.5%; Score 39; DB 70; Length 325; Best Local Similarity 75.3%; Pred. No. 1.36e-33; 09-JAN-1995 (Rel. 42, Created) 08-SEP-1995 (Rel. 45, Last updated, Version 2) The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878 80 t /organism="Homo sapiens" standard; RNA; EST; 325 BP. Location/Qualifiers 81 g (tdbinfo@tdb.tigr.org). /note="human" 92 c 103 TCTCTGTCCTCACCTG 119 Contact: Venter, JC 148 acceteteacteacetg 164 (bases 1 to 325) 58; Conservative Unpublished (1995) <1..>325 1..325NCBI gi: 611814 Fax: 3018699423 Tel: 3018699056 Homo sapiens 72 a LT 15 HS71611 T29716; ORGANISM BASE COUNT mRNA Matches REFERENCE AUTHORS JOURNAL FEATURES TITLE COMMENT RESULT ORIGIN

EST91759 Homo sapiens cDNA 5' end similar to immunoglobulin heavy chain V,D,J regions (GB:M34029) (HT:3782).

Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae. Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Homo sapiens (human)

Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A., Bult C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D., White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.W., Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D., FitzGerald L.M., FitzHugh W.M., Fritchman J.L., Geoghagen N.S.M., Glodek A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle Jr P.S., Kelley J.M., Klimek K.M., Kelley J.C., Liu L.I., Marmaros S.M., Merrick J.M., MORENO-PALANQUES R.F., McDonald L.A., Nguyen D.T., Pellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L.,
Saudek D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R.,
Weidman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A.,
Collana T.A., Collins E.J., Dimke D., Feng P., Ferrie A.,
Fischer C., Hastings G.A., He W.W., Hu J.S., Greene J.M.,
Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H.,
Meissner P.S., Olsen H., Raymond L., Wei Y.F., Wing J., Xu C.,
Yu G.L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A., Contact: Venter, JC The Institute for Genomic Research 932 Clopper and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org). NCBI gi: 611814 Rd, Gaithersburg, MD 20878 Tel: 3018699056 Fax: 3018699423 Email: tdbinfo@tdb.tigr.org For clone availability, additional sequence "Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence"; Haseltine W.A., Fields C., Fraser C.M., Venter J.C.; Location/Qualifiers

/organism="Homo sapiens" /note="human" Sequence 325 BP; 72 A; 92 C; 81 G; 80 T; 0 other;

0; Mismatches 19; Indels 0; Length 325; Query Match 9.5%; Score 39; DB 122; Best Local Similarity 75.3%; Pred. No. 1.36e-33; 58; Conservative

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ggtgtcctgtcacaattacagctgcagcagtcaggtccaggactggtgaagccctcgcag 147

acceteteacteacetg 164

Search completed: Mon Jul 8 09:06:44 1996 Job time : 199 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn Mon Jul 8 08:33:35 1996, MasPar time 33.32 Seconds 784.272 Million cell updates/sec Run on:

Tabular output not generated.

1 ATGGAGTCAGACACACTCCT......GGACCAAGCTGGAAATAAAA 393 TACCTCAGTCTGTGTGAGGA......cctgGTTCGACCTTTATTTT (1-393) from USO8137117B.seq 393 >US-08-137-117B-24 Description: Perfect Score: N.A. Sequence: Title:

TABLE default Scoring table:

Gap 6

Dbase 0; Query 0 STD: Nmatch

84802 seqs, 33246950 bases x 2 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

i.parti 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 n-geneseq22 Database:

Mean 8.287; Variance 5.196; scale 1.595 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.					1.81e-181			4.53e-176	
Description	p12-k2.	DNA encoding anti-idi	DNA encoding anti-idi	Mouse MAb 3B9 light c	Mouse antibody FB3-2	Mouse antibody F4-7 l	Vl coding sequence fr	Anti-CD4 antibody MT	p64-k4.
Œ	Q30753	090432	090431	083490	092501	092503	098534	609980	Q30757
h DB	5	16	16	14	16	16	16	9	2
% Duery Match Length	393	417	438	396	399	723	336	393	393
% Query Match	100.0	87.5	84.2	77.1	77.1	76.1	75.6	75.1	74.6
Score	393	344	331	303	303	599	297	295	293
Result No.	1	7	က	4	5	9	_	œ	σ,

g immunoq1 5.31e-170	mbryonic 5.31e-1	light ch 2.51e-1	light chai 5.59e-1	stimula 5.59e-	chain variable 1.24e-166		7.34e-	3.46e-		anti-idiot 3.60e-153				tibody lig 8.54e-148	HIV mu5.5 8.54e-148	1.88e-	immu 4.15e-	light cha 4.15e-145	able 9.	oi 9.12e-	6 4	o,	o 9.2.27 l 4.53e-1	the monoc 4.65e-1		variable 1.02e-1	1.02e-1	1.02e-1	1.10e-1	. 5	le 1	of 5.36e-1	8 A 1.06e-	antibody 3B 1.98e-90
DNA encoding DNA encoding	Anti-carcin	ly 4A	Murine 1B4	thyro	Light chain	Light chain variable	Porphyrin antibody	Mouse 0.5beta anti-HI	A V chi region gene	Mouse 4C10 anti-idiot	DNA encoding immunogl	DNA encoding anti-idi	Encodes kappa light	Anti HIV antibody lig	Mouse anti-HIV mu5.5	Human IgE r	Gene fragment of immu	Anti-Leu 3a light	Murine NM-01 variable	Human IgE r	Murine anti-CD18 Ab	Light chain variable	Chimeric MAb	Sequence of	Sequence of	Ξ.	Murine 1B4	_	Monoclonal		_	cha	sed	Humanized a
Q90421 Q90422	071394	034575	012683	074148	971286	204694	062631	025658	N90495	042987	030420	090430	Q10834	070372	065554	096285	N90492	004039	082818	096283	055002	073749	Q10379	056688	989950	049617	012684	037472	080292	8	097506	55	\sim	073986
16 16	12	9	7	16	12	-	Ξ	4		7	16	16					7		14		6	_	7	10	10	6	7	9	13	က	16	10	9	14
330 330	331	393	332	336	333	451	612	733	780	396	336	354	1014	333	333	336	334	006	333	336	334	334	336	363	363	334	336	363	645	312	336	309	334	393
73.8	72.8	72.5	72.0	72.0	71.5	71.0	67.4	67.2	67.2	66.4	65.1	65.1	65.1	64.4	64.4	63.9	63,4	63.4	62.8	62.8	61.8	61.3	61.1	<i>.</i>	60.3	9.	59.8	e.	ė.	54.7	53.7	51.1	46.1	42.5
290 286	286	282	283	283	281	279	265	264	264	261	256	256	256	253	253	251	249	249	247	247	243	241	240	237	237	235	235	235	223	215	211	201	181	167
11	12	13	14	15	16	11	18	19	20	21	22	23	24	52	56	27	58	59	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALI GNMENTS

Human, antibody, interleukin-6; receptor; IL-6R; light chain; L; H; heavy chain; variable region; mouse; monoclonal; hybridoma; AUK12-20; plasmid; pl2-k2; pl2-h2; ss. Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M; WPI; 92-398882/48.
P-PSDB; R28668.
Reconstituted human antibody to human interleukin-6 receptor Location/Qualifiers Q30753 standard; cDNA; 393 BP. 24-APR-1992; JO0544. 25-APR-1991; JP-095476. 19-FEB-1992; JP-032084. (CHUS) CHUGAI SEIXAKU KK. 30-MAR-1993 (first entry) /*tag= a mat_peptide /*tag= b W09219759-A. 12-NOV-1992. sig_peptide Synthetic. p12-k2. RESULT

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DR P-PSDB; R74967. PT Novel anti-idiotype antibody against an human anticancer monoclonal PT antibody - and DNA sequences encoding the antibody, useful in pharmacology, medicine and biochemical fields. PE Rample 5; Page 20; 28pp; Japanese. CC Q90425-Q90434 are DNA clones encoding anti-idiotype antibodies CC Q103, Idio17, Idio20, Idio27 and Idio33 against a human anticancer CC monoconal antibody. These antibodies and DNA encoding them are useful CC in pharmacological, medical and biochemical fields of research. SQ Sequence 417 BP; 100 A; 110 C; 113 G; 94 T;	Query Match 87.5%; Score 344; DB 16; Length 417; Best Local Similarity 95.7%; Pred. No. 3.41e-209; Matches 376; Conservative 0; Mismatches 14; Indels 3; Gaps 2.	Db 28 atggagacagacacctctgctatgggtactgctgtgttccaggttccaggttccaggt 87	Db 88 gacattgtgctgacacagtctcctgcttccttagctgtctctcggggcagacgcc 147	Db 148 atctcatacaggccagcaaaagtgtcagtacatctggctatagttatatgcactggaac 207	Db 208 caacagagaccaggacagccaccagactctcatctatcttgtatccaacctagactct 267	Db 268 ggggtccctgccaggttcagtggcagtgggtctgggacagattcacctcaacatccat 327	Db 328 cctdfggagagagatgctgcaacctattactgtcagcacttgagg-gagcttac 384	Db 385 acgttcggaggggaccaagctggaaataaaa 417 	RESULT 3 ID 200431 standard; DNA; 438 BP. AC 090431, DT 02-FEB-1996 (first entry) DE DNA encoding anti-diotype antibody Idio17 clone 17KB1. KW Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin; KW Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin; KW Complementarity determining region, ds. Nu sp. Location/Qualifiers FT Key Location/Qualifiers FT /*tag= a FT /*tag= b F
PT has low antigenicity and contains mouse V-region complementarity determining regions P3 biscloaure; Page 118; 207pp; Japanese. C5 The sequences given in Q30753-54 were used in example to illustrate C6 The sequences given in Q30753-54 were used in example to illustrate C7 the production of a human antibody which recognises human C8 interleukin-6 receptor (IL-68). The antibody comprises light (L) C8 contained heavy (H) chain variable regions which were derived from a C9 mouse monoclonal antibody produced from the hybridoma AUX12-20 which C9 contained the plasmids p12-k2 and p12-h2. S9 Sequence 393 BP; 98 A; 103 G; 103 G; 89 T;	Query Match 100.0%; Score 393; DB 5; Length 393; Best Local Similarity 100.0%; Pred. No. 2.00e-242; Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	<pre>Db 1 atggagtcagacactcctgctatgggtactgctgctcttgggttccaggttccactggt 60</pre>	Db 61 gacattgfgctgacacagtctcctggttccttagtgtatctctggggcaqagggccacc 120 	Db 121 atctcatgcagggccagcaaaatgtcagtacatctggctatagttatatgcactggtac 180 	Db 181 caacagaaaccaggacagcacccaaactcctcatctatct	Db 241 ggggtccctgccaggttcagtggcagtgggtctgggacagacttcaccctcaacatccat 300	Db 301 cctgtggaggaggatgctgcaacctattactgtcagcacagtaggagaatccgtac 360 	Db 361 acgttcggagggggaccaagctggaaataaaa 393 	RESULT 2 AC 090432 standard; DNA; 417 BP. AC 090432 DT 02-FEB-1996 (first entry) DE DNA encoding anti-idiotype antibody Idio20 clone 20KB1. DE DNA encoding anti-idiotype antibody Idio20 clone 20KB1. MA Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin; KW Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin; KW Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin; KW Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin; KW Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin; KW Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin; KW Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin; KW Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin; KW Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin; KW Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin; KW Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin; Location/Qualifiers ET /*tag= a FT /*tag= a FT /*tag= a FT /*tag= b FT /*tag

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임 요 ð g ð g δ 셤 ð g ð В δ à S '2 09045-090434 are DNA molecules encoding anti-idiotype antibodies Idio3, Idio17, Idio20, Idio27 and Idio33 against a human anticancer monoconal antibody. These antibodies and DNA encoding them are useful in pharmacological, medical and biochemical lields of research. Sequence 438 BP; 104 A; 120 C; 112 G; 102 T; 180 240 300 cctgcttccttagctgtatctctggggcagagggcctccatctcatacagggccagcaaa 120 141 261 357 201 321 381 9 81 Gaps Novel anti-idiotype antibody against an human anticancer monoclonal CCCAAACTCCTCATCTACCATCCAACCTAGAATCTGGGGTCCTGCCAGCTTCAGT gcaacctattactgtcagcacattaggg-gag--cttacacgttcggaggggggaccaag GCAACCTATTACTGTCAGCACAGTAGGGAGAATCCGTACACGTTCGGAGGGGGGGACCAAG ctatgggtactgctgctctgggttccaggttccactggtgacattgtgctgacacagtct agtgtcagtacatctggctatagttatatgcactggaaccaacagaaaccaggacagcca cccagactcctcatctatcttgtatccaacctagaatctggggtccctgccaggttcagt 0; Mismatches 10; Indels 3; antibody - and DNA sequences encoding the antibody, useful pharmacology, medicine and biochemical fields.

Example 5; Page 19; 28pp; Japanese. Chimeric antibody; humanized antibody; antibody engineering; monoclonal antibody; MAb; interleukin-4; IL-4; allergy; ds. Query Match 84.2%; Score 331; DB 16; Length 438; Best Local Similarity 96.5%; Pred. No. 2.15e-200; Location/Qualifiers 1..396 .T 4
Q83490 standard; cDNA; 396 BP 20-SEP-1995 (first entry) Mouse MAb 3B9 light chain. Conservative US-117366. US-136783. 1..60CTGGAATAAAA 393 ctggaaataaaa 369 U10308, 07-SEP-1993; 14-0CT-1993; 359; Q83490; 20-SEP-1995 07-SEP-1994; /*tag= a sig_peptide mat_peptide WO9507301-A 16-MAR-1995 ບ /*tag= b Mus sp. ---142 358 121 181 202 241 262 301 322 382 Matches 61 Key 음 g g 유 В 염 염 ð δ ð Š ò Š Š

Spleen cells from mice immunized with human IL-4 were used to prepare hybridomas, which were screened for anti-IL-4 Mbb secretion. Only clone 3B9 was positive. cDNA clones of the 3B9 light and heavy clairs were cloned into pGEM7f and transformed into E. coli DH5-alpha. The clones were sequenced (Q83490-91), and used for 240 300 301 CCTGTGGGGGGGGGGGTGCTGCTATTACTGTCACCACAGTAGGGAGAATCCGTAC 360 61 GACATTGTGGGGGCACAGTCTCCTTAGGTGTATCTCTGGGGCAGAGGGCCACC 120 121 atctoctgoaaggocagocaaagtgttgattatgatggtgatagttatatgaactggtac 180 cctgtggaggaggaggatgctgcaacctattactgtcagcaaagtaatgaggatcctccg 360 gacattgtgctgacccaatctccagcttctttggctgtgtctctagggcagagggccacc 120 9 9 Gaps caacagaaaccaggacagccaccaaactcctcatctatgctgcatccaatctagaatct gggatcccagccaggtttagtggcagtgggtctgggacagacttcaccctcaacatccat 241 GGGGTCCCTGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCAT 1 atggagacagacacaatcctgctatgggtgctgctgctctgggttccaggctccactggt Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated and IgE-mediated allergic conditions Disclosure; Fig.1; 97pp; English. ; 0 Score 303; DB 14; Length 396; 91 T; 0; Mismatches 45; Indels Match 77.1%; Score 303; DB 14; I Local Similarity 88.5%; Pred. No. 1.81e-181; 103 G; acgttcggtggaggcaccaagctggaaatcaaa 393 361 ACGTICGGAGGGGGGACCAAGCTGGAAATAAAA 393 103 C; DR; Holmes SD, Sylvester BEECHAM CORP BEECHAM PLC. BP. 99 A; Q92501 standard; cDNA; 399 348; Conservative antibody engineering. (SMIK) SMITHKLINE 396 BP; WPI; 95-123387/16. P-PSDB; R70189. Gross MS, Sequence Query Match Matches 61 181 181 241 301 361

variable region; antigen; immunorecessive; cell surface marker; foetal;

Mouse antibody FB3-2 light chain variable region coding sequence. Primer; amplification; PCR; mouse; kappa chain; heavy chain; Fab; antibody; immunotolerance; animal; variegated display library;

07-FEB-1996 (first entry)

cancer; stem cell; variant; therapy; Alzheimer's disease; hybridoma;

familial hypercholesterolaemia; binding affinity; ds

Mus musculus.

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Location/Qualifiers

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Q92503 standard; cDNA; 723 Local /*tag= Matches 67 181 음 ð 임 ð g õ 셤 074153-74. The variable regions, esp the complementarity determining regions (CDR; see R75462-93 for examples of CDRs) from the immunotolerant animals' antibodies are used to construct an antibody against a library (VDL) of variable regions derived from a repertoire of antibodies the variable regions from the antibody coding sequences using the primers 占 the antigen. The antibodies generated can be used in the diagnosis, e.g. detection of the immunorecessive antigen, or in therapy e.g. of cancer, Alzheimer's disease or familial hypercholesterolaemia. The method of antibodies produced have greater binding affinity than those produced by ö from an immunotolerised animal. The VDL is generated by PCR amplifying immunorecessive antigen e.g. a cell surface marker on a foetal, cancer stem cell, which can differentiate between variant or related forms of The coding sequence of the light chain variable region from the mouse antibody FB3-2. This sequence was isolated from a variegated display 67 gacattgtgatgacccagtctcctgcttccttagctgtatctctgggggcagagggccacc 126 GACATTGTGCTGACACACTCTCCTTGCTTAGGTGTATCTCTGGGGCCAGAGGGCCACC 120 127 atctcatgcagggccagccaaagtgtcagtacatctagatatagttatatgcactggtac 186 246 240 306 cctgtggaggaggatactgcaacatattactgtcagcacagttgggagattccgtac 366 CCTGTGGAGGAGGAGGATGCTGCAACCTATTACTGTCAGCACAGTAGGGAGAATCCGTAC 360 Gaps antibodies that would be difficult to isolate by standard methods. production of the antibody allows rapid and sensitive isolation of immuno:tolerance derived antibody repertoire, useful in diagnosis, caacagaaaccaggacagccaactcctcatcaagtttgcatccaacctagaatct 247 ggggtccctgccaggttcagtggcagtgggtctgggacagacttcaccctcaacatccat Generating new antibodies specific for immunorecessive epitopes by selection from variegated V gene library cloned from 0; Length 399; Indels 86 T; FB3-2 light chain variable region Copeland DP, Hillhouse D, Johnson T; 0; Mismatches 15; Score 303; DB 16; 1 Pred. No. 1.81e-181; 66 63 367 acgttcggaggggggaccaagctggaaataaaa 399 ACCTTCGGAGGGGGGCCCAAGCTGGAAATAAAA 393 purifcn, and therapy, e.g. of cancer Disclosure; Page 76-77; 109pp; English. 109 C; combinatorial/hybridoma methods. 105 A; 77.1%; 318; Conservative 08-DEC-1993; US-164022. 06-DEC-1994; US-350400. (GENZ) GENZYME CORP. 08-DEC-1994; U14106, Local Similarity /product= antibody 399 BP; Barsomian G, Cope. WPI; 95-224291/29. P-PSDB; R75457. WO9515982-A2 Sequence Query Match ع

Matches

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antibody F4-7. This sequence was isolated from a variegated display library (VDL) of variable regions derived from a repertoire of antibodies the variable regions from the antibody coding sequences using the primers stem cell, which can differentiate werecome the diagnosis, e.g. the antigen. The antibodies generated can be used in the diagnosis, e.g. detection of the immunorecessive antigen, or in therapy e.g. of cancer, regions (CDR; see R75462-93 for examples of CDRs) from the immunotolerant antibodies that would be difficult to isolate by standard methods. The antibodies produced have greater binding affinity than those produced by variable region; antigen; immunorecessive; cell surface marker; foetal; from an immunotolerised animal. The VDL is generated by PCR amplifying animals' antibodies are used to construct an antibody against a immunorecessive antigen e.g. a cell surface marker on a foetal, cancer stem cell, which can differentiate between variant or related forms of 61 GACATTGTGCTGACACAGTCTCCTGCTTCCTTAGGTGTATATCTCTGGGGCCAGAGGCCCACC 120 127 atctcatgcagggtcaggcaaagtgtcagtacatctagccatagttatatgcactggtac 186 121 ATCTCATGCAGGGCCAGCAAAAGTGTCAGTACATCTGGCTATAGTTATATGCACTGGTAC 180 The coding sequence of the light chain variable region from the mouse gacattgtgatgacccagtctcctgcttccttagctgtatctctggggcagagggccacc 126 247 ggggtccctgccaggttcagtggcagtgggtctgggacagacttcaccctcaacatccat 306 cancer; stem cell; variant; therapy; Alzheimer's disease; hybridoma; Q74153-74. The variable regions, esp the complementarity determining Gaps production of the antibody allows rapid and sensitive isolation of by selection from variegated V gene library cloned from immuno:tolerance derived antibody repertoire, useful in diagnosis, 187 caacagaaaccaggacagccacccaaactcctcatcaagtatgcatccaacctagaatct CAACAGAAACCAGGACAGCACCCAAACTCCTCCTTTGCATCCAACCTAGAATCT Primer; amplification; PCR; mouse; kappa chain; heavy chain; Fab; Generating new antibodies specific for immunorecessive epitopes 07-FEB-1996 (first entry) Mouse antibody F4-7 light chain variable region coding sequence antibody; immunotolerance; animal; variegated display library; 0 DB 16; Length 723; 151 T; 0; Mismatches 17; Indels Barsomian G, Copeland DP, Hillhouse D, Johnson T; WPI; 95-224291/29. P-PSDB; R75459. familial hypercholesterolaemia; binding affinity; ds /product= antibody F4-7 light chain variable region 172 G; Score 299; DB 16; Pred. No. 9.06e-179; Disclosure; Page 80-81; 109pp; English. 195 C; purifcn. and therapy, e.g. of cancer Location/Qualifiers combinatorial/hybridoma methods. 205 A; 76.18; 94.98; 316; Conservative 06-DEC-1994; US-350400. 08-DEC-1993; US-164022. (GENZ) GENZYME CORP 08-DEC-1994; U14106. Similarity 723 BP; MO9515982-A2. Mus musculus. 15-JUN-1995 Sequence Query Match

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cctgtggaggaggaggatgctgcaacctattactgtcagcacagtagggagtttccgtgg 300 301 CCTGTGGAGGAGGATGCTGCAACCTATTACTGTCAGCACAGTAGGGAGAATCCGTAC 360

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mouse-human antibody for diagnosis and treatment of cancer Claim 8; Page 16-17; 25pp; French. The nucleotide sequence of the variable region from the light chain of an antibody against cancer-specific mucin. The coding sequence was isolated from Nd2 hybridoma cells expressing a murine antibody reactive with
                                                                                                                                                                                                                                                                                              VI coding sequence from an antibody against cancer-specific mucin.
Antibody; heavy chain; light chain; variable region; cancer; mucin;
hybridoma cell; murine; mouse; pancreatic cancer cell; expression vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the detection and treatment of cancer. The chimeras should be less likely to cause anaphilaxis than the original murine antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from the heavy (Q98533) and light chains were isolated and inserted into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pancreatic cancer cells. The DNA encoding the antibody variable regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    These vectors express the domains as an Fv antibody. Vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   which additionally contain genes encoding the human constant domains express a chimeric mouse-human antibody. The antibodies are useful in
                                                                        241 GGGTCCCTGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCAT 300
                                                      307 cctgtggaggaggaggatactgcaacatattactgtcagcacagttgggagattccgtac 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; R80272.
New variable domains of antibody recognising cancer specific mucin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - and related DNA and expression vectors, producing chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 75.6%; Score 297; DB 16; Length 336;
Best Local Similarity 94.6%; Pred. No. 2.03e-177;
                                                                                                                                                                                                                                                                                                                                                       Fv; human; constant domain; chimera; anaphilaxis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chung Y, Iba Y, Kaneko T, Sowa M, Yasukawa K;
WPI; 95-247908/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 G;
                                                                                                                         express a chimeric mouse-human antibody.
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                                                                                                                                                                                                                                         Q98534 standard; DNA; 336 BP.
                                                                                                                                                                                                                                                                           27-FEB-1996 (first entry)
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misc_feature 277..303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160..180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc difference 190..192
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13-JAN-1994; JP-002131.
                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/note= "encodes CDR1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "encodes CDR3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc feature
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                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
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immunosuppression; tissue transplantation; graft; L chain; V region; T-helper cell inhibition; transplant rejection; MAb;

Location/Qualifiers

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sig peptide mat_peptide

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interleukin-2 receptor; ss.

02-JUN-1993 (first entry) Anti-CD4 antibody MT 3.10 light chain variable region.

.r 8 Q36609 standard; DNA; 393 BP.

DB 6; Length 393; 90 T; Query Match 75.1%; Score 295; DB 6; L Best Local Similarity 87.5%; Pred. No. 4.53e-176; 98 G; 105 C; 100 A; 393 BP; Sequence **;** 1 gacattgtgctgacacagtctcctgcttccttagctgtatctctggggcagagggccacc 60 Gaps 0;

0; Mismatches 18; Indels

Matches 315; Conservative

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Claim 5; Page 11; 18pp; German.
This sequence encodes the light chain variable region of a preferred anti-CD4 monoclonal antibody for use in the claimed synergistic composition. MAb MT 3.10 is deposited as clone 3.101/sB10 (ECACC

comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R

alpha- or anti-IL2R beta antibodies

Synergistic antibody compsn. for use as immunosuppressant

Kaluza B, Riethmueller G, Scheuer W, Weidle U;

WPI; 93-037582/05.

P-PSDB; R32123.

30-DEC-1991; DE-143214. (BOEF) BOEHRINGER MANNHEIM GMBH.

25-JUL-1991; DE-124759.

30-DEC-1991; 143214.

/note= "J1 region begins at position 361"

DE4143214-A.

/*tag=

28-JAN-1993

61..393

90090702). The anti-CD4 antibody is used with at least one anti-IL2R inhibiting and when used together their immunosuppressive properties

alpha or beta antibody. Individually the antibodies are strongly

doses without significantly reducing the general immune response. See Q36607-Q36616.

proliferation to effectively inhibit transplant rejection at low

are improved; they synergistically inhibit T-helper cell

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anti-idiotype antibody against a human anticancer monoconal antibody. This antibody contains in its heavy chain 3 complemetarity determining regions CDR1 (R74929-R74931), CDR2 (R74932-R794935) and CDR3 (R74936-R74939), this is also true of the light chain which has its own CDR1 (R74950-R74954) ö Claim 19; Page 5; 28pp; Japanese. 090420-090424 are DNA molecules encoding possible light chains of a new The antibody and DNA encoding it are useful in pharmacological, medical and biochemical fields. cagcagaaaccaggacagccacccaaactcctcatctatcgtgcatccaacctagaatct 240 gacattgtgttgatccaatctccagcttctttggctgtgtctctagggcagagggccacc 120 121 atatoctgcagagocagtgaaagtgttgatagttatggcaatagttttatgcactggtac 180 121 ATCTCATGCAGGCCCAGCAAAAGTGTCAGTACATCTGGCTATAGCTTATATGCACTGGTAC 180 gggatccctgccaggttcagtggcagtgggtctaggacagacttcaccctcaccattaat 300 300 cctgtggaggctgatgatgttgcaacctattactgtcagcaaagtaatgaggatcctccc 360 301 ccreregaegaegarecrecaactarracreregaegaragegagarrecerac 360 9 9 Gaps Novel anti-idiotype antibody against an human anticancer monoclonal GGGGTCCCTGCCAGGTTCAGTGGCAGTGGGACAGACTTCACCCTCAACATCCAT 1 atggagtcagacacactcctgctatgggtgctgctgctgggttccaggttccacaggt DNA encoding immunoglobulin light chain of anti-idiotype antibody Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin; .**,** antibody - and DNA sequences encoding the antibody, useful CDR2 (R74947-R74949) and CDR3 Length 393, 0; Mismatches 50; Indels Ë 66 74 Score 293; DB 5; L. Pred. No. 1.01e-174; 100 G; ċ pharmacology, medicine and biochemical fields 85 361 ACGTTCGGAGGGGGACCAAGCTGGAAATAAAA 393 361 acgttcggtgctgggaccaagctggagctgaaa 393 101 C; ن complementarity determining region; 98 against human anticancer antibody Ξ (R74944-R74946 and R85774), 85 A; Ä 74.6%; 87.3%; 19-JAN-1996 (first entry) JT 10 Q90421 standard; DNA; 330 343; Conservative 93 18-APR-1995. 06-OCT-1993; 272950. 06-OCT-1993; JP-272950. (HAGI/) HAGIWARA Y. WPI; 95-182987/24. Query Match Best Local Similarity 330 BP; BP; P-PSDB; R74956. 393 J07101999-A Sequence Sequence

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61 atctcatacagggccagcaaaagtgtcagtacatctggctatagttatatgcactggaac 120
                                                                                           cctgtggaggaggaggatgctgcaacctattactgtcagcacattgagg-gag--cttac 297
                                                                                                                                                                                                                                                                                                                       antigen during therapy. It can also be used in vivo diagnostically,
                                                                                                                                                                                                                                                               241 GGGGTCCCTGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCAT
                                                                                                                                                                                                                            for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-carcinoembryonic antigen chimeric antibodies — for diagno
and therapy of carcinoma, e.g. breast or colorectal carcinoma
Claim 1; Page 49; 67pp; English.
Q71394 codes for R60564 the antibody light chain region of
                                                                                                                                                                     Score 286; DB 12; Length 331;
Pred. No. 5.31e-170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        murine-human anti-carcinoembryonic antigen (CEA) chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibody. Which can be used in in vitro immunoassays for the detection of CEA, and monitoring of tumour-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-carcinoembryonic antigen chimeric light chain Ab, cE
Anti-carcinoembryonic antigen chimeric antibodies; CEAS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chimeric human-murine; breast or colorectal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for the treatment of tumours associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      colorectal and breast carcinomas, as well those of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lung, ovary and pancreas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICES.
Gourlie BB, Kaplan DA, Mezes PS, Rixon MW,
                                                                                                                                                                                                                                                                                                                                                                                               361 ACCTTCCCAGGGGGCCCAACTAGAA 393
                                                                                                                                                                                                                                                                                                                                                                            298 acgttcggagggggaccaagctggaaataaaa 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q71394 standard; cDNA; 331 BP
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95.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric Mus muscaris.
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16-FEB-1994; U01709.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            light chain; ds.
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WO9419466-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anti-idiotype antibody against a human anticancer monoconal antibody. This antibody contains in its heavy chain 3 complemetarity determining regions CDR1 (R74929-R74931), CDR2 (R74932-R794935) and CDR3 (R74936-R74939), this is also true of the light chain which has its own CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (R74944-R74946 and R85774), CDR2 (R74947-R74949) and CDR3 (R74950-R74954)
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                                                      5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The antibody and DNA encoding it are useful in pharmacological, medical
                                                                                                              61 GACATTGTGCTGACAGTCTCCTGCTTCCTTAGGTGTATCTCTGGGGCCAGAGGCCCACC 120
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                                                                                                                                                                                                                                                                                                                                                                                            atctcatacagggccagcaaaagtgtgagtacatctggctatagttatatgcactggaac 120
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                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel anti-idiotype antibody against an human anticancer monoclonal antibody - and DNA sequences encoding the antibody, useful in pharmacology, medicine and biochemical fields.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encoding immunoglobulin light chain of anti-idiotype antibody.
                                                                                                                                                                                                                                                                               CAACAGAAACCAGGACAGACACCCCAAACTCCTCATCTTGCATCCAACCTAGAATCT
                                                                                                                                                                                                                                                               against human anticancer antibody.
Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; Page 5; 28pp; Japanese.
090420-090424 are DNA molecules encoding possible light chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
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                 Length 330,
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                                                      0; Mismatches 11; Indels
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Pred. No. 5.31e-170;
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                                 Pred. No. 1.07e-172;
               Score 290; DB 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complementarity determining region;
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               73.8%;
95.8%;
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Best Local Similarity 95.2%;
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                                                    Matches 319; Conservative
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06-0CT-1993; JP-272950.
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٥y	181 CAACAGAAACCAGGACAGACACCCAAACTCCTCATCTTGCATCCAACCTAGAATCT 240	
QQ	241 ggggtcctgcaggtttagtggcagtgggtctgggacagacttcagcctcaacatccat 300	
٥y	241 GEGGTCCTGCCAGGTTCACTGCCAGTGCGTCTGGGACTTCACCCTCAACATCCAT 300	
qq	301 cctgtgggggaggaggatattgcgatgtatttctgtcagcagagtaggaaggttccttgg 360	
δy	301 CCTGTGGAGGAGGATGCTGGAACCTATTACTGTCAGGAGAGAGA	
QQ	361 acgttcggtggagcaccaagctggaaatcaaa 393	
Qγ	361 ACGTTCGCAGGGGGCCCCAACCTGGAAATAAAA 393	
REŚ	SULT 14	
ID A	Q12683 standard; DNA; 335 BP. 012683:	
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2	integrin, hybridoma 1B4; protein REI; Gal/Rei; Ig; ss.	
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7. Z	19-0AN-1990; 0S-46/692. 20-DEC-1990: US-627421.	
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ည (human myeloma protein REI (EP-239400).	
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ž	sequence 333 Br; 61 B; 69 C; 63 G;	
α m	Query Match 72.0%; Score 283; DB 2; Length 335; Best Local Similarity 95.5%: Pred. No. 5.59e-168:	
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Op	1	
Qy	61 GACATTGTGCTGACACACTCCTGCTTTAGGTGTATCTGTGGGGGAGAGGGCCACC 120	
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11 Qy	181 GANGGAMCCAGACACACACACACACACACACACACACACACAC
Db 121	
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	vancadanaccadencadacacconnaciccicaiciaiciiacciccancciadanici
Db 181	. ggggtccctgccaggttcagtggcagtgggtctgggacagacttcaccctcaacatccat 240
	GCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
Qy 241	GGGGTCCCTGCCAGGTTCAGTGGGTGTGGGTCTGGGACAGACTTCACCCTCAACATCCAT 300

241 cctgtggaggacgatgctgcaacatattactgtcaacacacttgggagattcctcgg	300	
241 cctgtggaggaggacgatgctgcacatatt:	ggagattcc	
241 cctgtggaggaggacgatgctgcacatat	ta	Ξ
241 cctgtggaggaggacgatgctgcaaca	atat	Ξ
241 cctgtggaggaggacgatgctgc	aac	Ξ
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Search completed: Mon Jul 8 08:34:22 1996 Job time : 47 secs.

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SUMMARIES

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(ML)

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

Mon Jul 8 08:27:26 1996; MasPar time 264.76 Seconds 1050.869 Million cell updates/sec

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn

Tabular output not generated.

Run on:

(1-393) from USO8137117B.seq 393 >US-08-137-117B-24 Description: Title:

Perfect Score:

1 ATGGAGTCAGACACACTCCT......GGACCAAGCTGGAAATAAAA 393 N.A. Sequence:

TACCTCAGTCTGTGTGAGGA.......cctggttcgacctttattt

TABLE default Scoring table:

Gap 6

Dbase 0; Query 0 •• STD Nmatch 264399 seqs, 353985056 bases x 2 Searched:

Minimum Match 0% Post-processing:

Listing first 45 summaries

Database:

embl-newil 1:BCT 2:FUN 3:INV1 4:INV2 5:INV3 6:MAM 7:ORG 8:PLN 9:PRII 10:PRI2 11:PRI3 12:PRO1 13:PRO2 14:ROD 15:SYN 16:UNC 17:VRT 18:VIR

Database:

genbank91
19:BCT1 20:BCT2 21:BCT3 22:BCT4 23:BCT5 24:BCT6 25:BCT7
26:INV1 27:INV2 28:INV3 29:INV4 30:INV5 31:BAM1 32:BAM2
33:PAT1 34:PAT2 35:PAT3 36:PHG 37:PLN1 38:PIN2 39:PLN3
40:PLN4 41:PLN5 42:PLN6 43:PLN7 44:PRT1 45:PRT2 46:PRT3
47:PRT4 48:PRT5 49:PRT6 50:PRT7 51:PRT8 52:PRT9 53:ROD1
54:ROD2 55:ROD3 56:ROD4 57:ROD5 58:ROD6 59:ROD7 60:STR 61:SYN 62:UNA 63:VRL1 64:VRL2 65:VRL3 66:VRL4 67:VRL5

68:VRL6 69:VRT1 70:VRT2 71:VRT3 genbank-new11 Database:

72:BCT1 73:BCT2 74:INV1 75:INV2 76:MAM 77:PHG 78:PLN 79:PR11 80:PR12 81:PR13 82:ROD 83:STR 84:SYN 85:UNA

86:VRL 87:VRT u-emb144 91

88:part1 Database:

Mean 10.331; Variance 3.912; scale 2.641 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mus musculus (strain A/J, sub_species domesticus) hyperimmunized spleen cDNA to mRNA.

Mus musculus

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;

ORGANISM

SOURCE

MUSIGLCUX 393 bp mRNA ROD 02-MAY-1994 Mouse immunoglobulin light chain variable region mRNA, 5' end. L31404

ALIGNMENTS

immunoglobulin light chain; variable region.

DEFINITION ACCESSION KEYWORDS

RESULT

LOCUS

		Onerv					
Result No.	Score	Match	Length	DB	aı	Description	Pred. No.
			-			1	- 1
-	355	90.3	393	26	MUSIGLCVX	noglob	•
7	320	89.1	390	14	MMIGKV3B6	mRNA for	•
m	320	89.1	330	82	MMI GKV3B6	M.musculus mRNA for I	0.00e+00
4	345	87.8	429	54	MMI GVKP	핕	0.00e+00
5	345	81.8	444	26	MUS I GKCSU	Mouse Ig aberrantly r	0.00e+00
9	345	87.8	526	96	MUSICKPSV	Mus musculus processe	0.00e+00
7	312	79.4	336	96	MUS I GKADK	Mouse Ig rearranged k	0.00e+00
00	307	78.1	333	54	MMT 3VL	M. musculus anti-T3 9	1.25e-297
6	306	77.9	9	54	MMI GVK20P	M.musculus Iq Vkappa-	1.61e-296
10	305	77.6	106		MUSIGKVR1	Mouse Ig germline kap	2.07e-295
Ξ	303	77.1	999		MMIG21E5	Id	3.42e-293
12	301	76.6	333	53	MDIGKVBI	sťi	5.65e-291
13	300	76.3	333		MMVL103	Mouse mRNA for kappa-	7.26e-290
14	299	76.1	394	2	MMU 0 1 9 7 3	Mus musculus Balb/c a	9.33e-289
15	296	75.3	339	99	MUS I GKAAS	Mouse immunoglobulin	N
16	295	75.1	332	5	MMI GGL3	Mus musculus (DBA/1)	.53e-
17	295	75.1	333	Ş	MDIGKVCC	mesticus	.53e-
18	295	75.1	393	5	\$50265	۵	.53e-
19	291	74.0	333	5	MMU25122	Mus musculus anti-sta	.85e-
20	291	74.0	393	2	MUSIGKM195	musculus IqK cha	.85e-
21	291	74.0	633		MUSIKC	musculus	85e-
22	290	73.8	330	5	MMIG2832K	M.musculus mRNA for a	8.77e-279
23	287	73.0	309	29	S67895		1.84e-275
24	287	73.0	706	2	MUSICKVQ	Mouse Ig germline kap	.84e-
25	285	72.5	330		MUS I GKCVAA	Mus musculus immunogl	.01e-27
26	285		336		MUSANTDNAB	Mouse anti-DNA antibo	3.01e-273
27	283		333		MUSIGKVBA	Mouse Ig rearranged k	4.93e-271
28	282	•	333		MUSIGVLA	Mus musculus Ig light	6.30e-270
59	281	71.5	327		574564	Ig V kappa =rheumatoi	8.04e-269
30	281	-	333		MMU23048	Mus musculus clone H2	8.04e-269
31	280	71.2	323	99	MUS I GKADH	Mouse Ig rearranged k	1.03e - 267
32	279	71.0	451		A07951	Artificial sequence f	.31e-
33	279		469		MUSIGKBK	Mouse Iq aberrantly r	.31e-
34	277	70.5	999	2	MUSIGLBPA	Mouse mRNA for immuno	2.14e-264
35	275		312	5	260870	Ab2 kappa chain V reg	3.47e-262
36	272	œ.	720	S	569214		7,18e-259
37	271	-	396		SYN4C10L	Murine/Human chimeric	4e-
38	566	٠.	306	3	MMA 60L	M.musculus immunoglob	.04e-2
39	566	67.7	306	Т	MMA 60L	M.musculus immunoglob	
40	566	67.7	909	5	MUSIGVLAA	Mouse Ig L-chain gene	3.04e-252
41	265	67.4	333	5	S74543	Iq V kappa =rheumatoi	3.86e-251
42	264	67.2	306	53	MMA 7 L	M.musculus immunoqlob	4.91e-250
43	264	67.2	306	14	MMA 7L		4.91e-250
44	263	6.99	287	5	MMVKBWA2	-	23

US-08-137-117B-24.gg

Rodentia; Myomorpha; Muridae; Murinae

Eutheria;

REFERENCE AUTHORS sig_peptide

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Query Match

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61 gacattgtgctgacacagt	. GACATTGTGCTGACACAG
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379; Conservative 225..240 340..360 partial ..>390 1..390 . 9 Mus musculus (mouse) Local Similarity kappa light chain BP; Rosell-Vives E.; Sequence 390 sig_peptide CDS misc_feature misc feature misc_feature Jnpublished receptor. V_region Query Match source 1 - 390Matches Best 9 δ /translation="METDT1LILMVILLAVPESTGDIVLTQSPASIAVSIGGRATISCR ASKSVSTSGYSHIHWYQQKPQQPPKLLIYLASILESGVPARFSGSGSGTDFTLAIHPV EEEDAATYYCQHSREYPLTFGAGTELEIK" Jeffrey, P.D., Schildbach, J.F., Chang, C.Y., Kussie, P.H., Sheriff, S. and Margolies, M.N. ; 0 121 atctcatgcagggccagcaaaagtgtcagtacatctggctatagtcatatacactggtac 180 240 300 GGGGTCCCTGCCAGGTTCAGTGGCAGTCTGGGACAGACTTCACCCTCAACATCCAT 300 cctgtggaggaggatgctgcaacctattactgtcaacacagtagggaatatccgctc 360 /codon_start=1 /product="immunoglobulin light chain variable region" 9 9 Gaps Structure and specificity of the anti-digoxin antibody 40-50 Unpublished (1994) 1 ATGGAGTCAGACACACTCCTGCTATGGGTACTGCTGTGCTCTGGGTTCCAGGTTCCACGGT ggggtccctgccaggttcagtggcagtggctgggacagacttcaccctcaacatccat 1 atggagacagacactcctgttatgggtactgctgctctgggttccaggttccactggt ö Length 393, 0; Mismatches 19; Indels /tissue_type="hyperimmunized spleen" Score 355; DB 56; Pred. No. 0.00e+00; /sub species="domesticus" /cell type="hybridoma" /sequenced mol="cDNA to mRNA" 361 acgttcggtgctgggaccgagctggagctgaaa 393 ACCTTCGGAGGGGGACCAAGCTGGAAATAAAA 393 organism="Mus musculus" /note="NCBI gi: 476720" 100 g Location/Qualifiers /codon_start=1 /strain="A/J" /codon_start= 90.3**%**; 95.2**%**; 108 c 374; Conservative (bases 1 to 393) MMIGKV3B6 standard; RNP NCBI gi: 476719 1..393Best Local Similarity 93

/cell_type="fusion of splenocytes x HL1 friendly myeloma 8 Gaps 29-SEP-1995 (Rel. 45, Created) 24-OCT-1995 (Rel. 45, Last updated, Version 4) M.musculus mRNA for Ig kappa light chain variable region (cell line complementarity determining region; immunoglobulin variable region; region of Ig kappa light chain" 1 atggagtcagacacactcctgctatgggtactgctgctctgggttccaggttccactggt Ë Piulats J.; "Immunological and structural properties of anti-idiotypic antibodies mimicking an epitope of human epidermal growth factor E. Rosell-Vives, MERCK, Farma y Quimica S.A., Caspe 108, E-08010 Barcelona, SPAIN .; : Carceller A., Rosell-Vives E., Gomez-Roig A., Adan J., Sproll Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; 5 3 /product="immunoglobulin kappa light chain" /note="pid:e200732" Score 350; DB 14; Length 390; Pred. No. 0.00e+00; 0; Mismatches 11; Indels Submitted (19-SEP-1995) to the EMBL/GenBank/DDBJ databases. /note="complementarity-determining region 96 A; 103 C; 100 G; 91 T; 0 other; /note="complementarity-determining region /note="complementarity-determining region Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae US-08-137-117B-24 rge /tissue_type="hybridoma" /organism="Mus musculus" /sub_strain="by J Ico" Location/Qualifiers 'product="variable /strain="BALB/c" /cell line="3B6" /product="CDR3" /product="CDR1" /product="CDR2" chromosome="6" 89.1%; 96.4%; (Rel. 45, (Rel. 45, 1 29-SEP-1995 24-OCT-1995

US-08-137-117B-24.rge

ASKSVSTSGYSYMHWNQQKPGQPPRLLIYLVSNLESGVPARFSGSGSGTDFTLNIHPV EEEDASTYYCQHIREVYTFGGGTKLEIK" V_region 1390 /product="variable region of Iq kappa light chain"	; ;	region	/note= complementarity-determining region 2 /product="CDR2" misc_feature 340360 /note="complementarity-determining region 3" /noduct="CDR3"	BASE COUNT 96 a 103 c 100 g 91 t	Query Match 89.1%; Score 350; DB 82; Length 390; Best Local Similarity 96.4%; Pred. No. 0.00e+00; Matches 379; Conservative 0; Mismatches 11; Indels 3; Gaps 2;	Db 1 atggagtdagacacactcctgctatgggtactgctgtgggttccaggttccactggt 60	Db 61 gacattgtgctgacacagtctccttgcttccttagctgtatctctggggccagagggccacc 120	61 GACATTGTGCTGACACAGTCTCCTTGCTTAGGTGTATCTCTGGGGGGGG	DD 121 accidatacagggccagcaaaqtqrcagtacatcgggctataqtatcqcactggaac 180	181 caacagaaaccaggacagccaccagactcctcatctatct	Qy 181 CAACAGAACCAGGACAGACCCCAAACTCCTCATCTTTCTT	Db 241 ggggtcctgccaggttcagtggcagtgggtctgggacagatttcacctcaacatccat 300	Db 301 cctgtggaggaggatgcctcaacctattactgtcagcacattagggagg-tctac 357	Qy 301 CCTGTGGGGGGGGGGGGTGCTGCAACTATTACTGTCAGCACAGTAGGGAATCCGTAC 360	361 ACTTCGAGGGGGGCACCAACTGGAAATAAAA		RESULT 4 LOCUS MMIGVKP 429 bp RNA ROD 04-AUG-1992 LOCUS DEFINITION Mouse mRNA for nonfunctionally rearranged Ig-kappa V/Jk2 region. ACCESSION X05184 M31709 KEYMORDS IG kappa Light chain; Ig light chain. SOURCE house mouse.	ORGANISM Mus musculus Eukaryotae; Mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bulateria; Ocelomata; Deuterostomia; Chordata; Vortobrata: Carbotamata; Ontociathbus; Sarototoria; Chanata;	REFERENCE 1 (Dages 1 CO 42) AUTHORS Strohal,R., Kroemer,G., Wick,G. and Kofler,R. TITLE Complete variable region sequence of a nonfunctionally rearranged
Db 121 atctcatacagggccagcaaaadtgtcagtacatctggctatagttatatgcactggaac 180 		<pre>UD 181 caacaggaacagccacccagactcctcatctatctgtatccaacctagaacct 440</pre>	Db 241 ggggtccctgccaggttcagtggcagtgggtctgggacagatttcacctcaacatccat 300	Db 301 cctgtggaggaggaggatgcctcaacctattactgtcagcacattagggagg-tctac 357	358	3	LOCUS MEMICANISES 390 DP KNA DEFINITION M.msculus mRNA for Ig kappa light chain variable region (cell line 386).	ACCESSION X91670 KEYWORDS complementarity determining region;	Immunodicoulin variable region; Kappa lignt cnain. SOURCE house mouse. ORGANISM Mus musculus		REFERENCE 1 (bases 1 to 390) AUTHORS Carceller, A., Rosell-Vives, E., Gomez-Roig, A., Adan, J., Sproll, M.	and Piulats, J. TITLE Immunological and structural properties of anti-idiotypic antibodies mimicking an epitope of human epidermal growth factor	JOURNAL Geceptor JOURNAL Unpublished REFERENCE 2 (bases 1 to 390)	Rosell-Vives, E. Direct Submission Submitted 410_crp_1065 + + to EMBI /Condont /NDDI	2	COMMENT NUBL 91: 1001882 FEATURES Location/Qualifiers	source 1390 /organism="Mus musculus" /strain="BALB/c" /sub_strain="by J Ico" /tissue_type="hybridoma" /cell_type="fusion of splenocytes x Hil friendly myeloma	653" /cell line="386" /chromosome="6"	/codon_start=1 /product="immunoglobulin kappa light chain" /translation="MESDTLLLMVPGSTGDIVLTQSPASLAVSLGQRATISYR

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cctgtggaggaggatgctgcaacctattactgtcagcacattagggagc-t---tac 383 ggggtccctgccaggttcagtggcagtgggtctgggacagacttcaccctcaacatccat 241 GGGGTCCCTGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACCTCAACATCCAT acgttcggagggggaccaagctggaaataaaa 416 ACGTTCGGAGGGGGACCAAGCTGGAAATAAAA 393 sig peptide mat_peptide Query Match source BASE COUNT ORGANISM Matches 61 121 208 268 328 301 384 181 361 JOURNAL AUTHORS MEDLINE REFERENCE S FEATURES TITLE COMMENT ORIGIN RESULT SOURCE g ð g δ 셤 ð g 셤 ð 염 ð g à δ 2; appa light chain transcribed in the nonsecretor P3-X63-Aq8.65 220 280 340 300 cctgtggaggaggatgctgcaacctattactgtcagcacattagggagc~t---tac 396 41 atggagacagacacactcctgttatgggtactgctgctctgggttccaggttccactggt 100 CCTGTGGAGGAGGAGGATGCTGCAACCTATTACTGTCAGCACAGTAGGGAGAATCCGTAC 360 9 Mouse Ig aberrantly rearranged kappa-chain mRNA V-J2-C-region complete cds. 12-JUN-1993 the Balb/c Gaps 161 atctcatacaggccagcaaaagtgtcagtacatctggctatagttatatgcactggaac ggggtccctgccaggttcagtggcagtgggtctgggacagacttcaccctcaacatccat caacagaaaccaggacaacccagactcctcatctatcttgtatccaacctagaatct C-region; J-region; V-region; immunoglobulin light chain; 4. Length 429 ဌ 0; Mismatches 10; Indels The nonfunctional transcript shows 98% homology to -1)" Data kindly reviewed (18-May-1988) by Strohal /cell_line="myeloma P3-x63-Ag8.653" Score 345; DB 54; Pred. No. 0.00e+00; -20 /note="out of frame joint" 116 c 107 g 98 397 acgttcggaggggggaccaagctggaaataaaa 429 /note="primary transcript" /note="leader peptide (AA /organism="Mus musculus" Nucleic Acids Res. 15 (6), 2771 mRNA Location/Qualifiers /note="Vk segment" /strain="Balb/C" 444 bp Vk21-E germline gene Query Match 87.8%; Best Local Similarity 96.4%; 379; Conservative 101..393 393..394 myeloma cell line $1..>4\overline{2}9$ 41..100 1..429 æ MUSICKCSU NCBI gi: prim_transcript 87174798 108 misc_feature misc_feature misc_feature Ŋ BASE COUNT ORIGIN source Matches DEFINITION 301 361 101 61 121 221 181 281 241 341 ACCESSION JOURNAL MEDLINE KEYWORDS FEATURES RESULT LOCUS g 셤 P 음 g à à 셤 임 ò õ ò ò à

/translation="METDTLLLMVLLLWVPGSTGDIVLTQSPASLAVSLGQRATISYR ASKSVSTSGYSYMHWNQXPGQPPRLLIYLVSNLESGVPARFSGSGSGTDFTLNIHPV gi: 2; Hybridoma fusion cell lines contain an aberrant kappa transcript Mol. Immunol. 25, 991-995 (1988) 88 gacattgtgctgacacagtctcctgcttccttagctgtatctctggggcagagggccacc 147 NCBI GACATTGTGCTGACACACTCTCCTTCCTTAGGTGTATCTCTGGGGCAGAGGGCCACC 120 148 atctcatacaggccagcaaaagtgtcagtacatctggctatagttatatgcactggaac 207 81 9 Gaps Theria; /note="Ig kappa-chain V-J2-C-region signal peptide" 28 atggagacagacactcctgttatgggtactgctgctcgggttccaggttccactggt 1 ATGCAGTCAGACACACTCCTGCTATGGGTACTGCTGCTTCTGGGTTCCAGGTTCCACTGGT /note="Ig kappa-chain V-J2-C-region precursor; 309369" 4; Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Score 345; DB 56; Length 444; Pred. No. 0.00e+00; Indels Eutheria; Rodentia; Myomorpha; Muridae; Murinae /note="Ig kappa-chain V-J2-C-region" /codon_start=1 0; Mismatches 10; immunoglobulin-kappa. Mouse myeloma MOPC-21, cDNA to mRNA. 103 EEEDAATYYCQHIRELTRSEGGPSWK Carroll, W.L., Mendel, E. and Levy, S. /organism="Mus musculus" 28..87 Location/Qualifiers 111 g /codon start=1 /codon start=1 87.8%; Local Similarity 96.4%; les 379; Conservative 122 c 1 (bases 1 to 444) $28..41\overline{4}$ 1..444 88..411 NCBI gi: 197295 108 a Chromosome 6. Mus musculus 89112230

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DEFINITION

ACCESSION

KEYWORDS

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FEATURES COMMENT

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BASE COUNT ORIGIN

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/codon_start=1 /translation="DIVLTQSPASLPVFLGQRATISCRASKSVGISDYSYMHWYQQKP GQSPKLLIYLASNLESGVPXRFSXSGSGTDFTLNIHPVEEEDAATYYCQHSRELPYTF J-region, V-region; immunoglobulin light chain; processed gene. Mouse (strain Balb/c), cDNA to mRNA, anti-influenza hemagglutinin hybridoma H37-68 Vk. Draft entry and computer-readable sequence for [J. Immunol. (1990) ÷ Clarke, S.H., Rickert, R., Wloch, M.K., Staudt, L.M., Gerhard, W. and Sb site of influenza virus 61 atctcatgcagggccagcaaaagtgtcggtatatctgactatatgttatatgcactggtac 120 61 GACATTGTGCTGACACAGTCTCCTGCTTCCTTAGGTGTATCTCTGGGGCAGAGGGCCACC 120 121 ATCTCATGCAGGCCAGCAAAAGTGTCAGTACATCTGGCTATAGTTATATGCACTGGTAC 180 338 ggggtccctgccaggttcagtggcagtgggtctgggacagacttcaccctcaacatccat 397 cctgtggaggaggaggatgctgcaacctattactgtcagcacattagggagc-t---tac 453 9 24-JUL-1990 Gaps Mouse Ig rearranged kappa-chain mRNA V-J region, partial cds. Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; 1 gacattgtgctgacacagtctcctgcttccttacctgtatttctggggcagagggccacc /note="Ig H-chain V-J-region; NCBI gi: 196610" .; 0 Score 312; DB 56; Length 336; Pred. No. 0.00e+00; 3 others 0; Mismatches 12; Indels Eutheria; Rodentia; Myomorpha; Muridae; Murinae 염

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	octatadadaadaatactacaacctatactatcacacaatadaaacttccatac	δλ	301 ccrerc	ccrerceage
	CCTCTCGGAGGAGGAGGATCCTGCAACCTATTACTGTCACCACACAGGAGAGAATCCCTAC	qa		acgttcggtgg
Db 301	1 acgttcggagggggaccaagctggaaataaaa 333	δλ	361 ACGTTCGGAGG	CGGAGG
0у 36	361 ACGTICGGAGGGGGGCTCGAATAAAA 393	RESULT	6	MM I CVK 2 0P
e made	o	DEFINITION		M. musculu
LOCUS DEFINITION	MMT3VL 333 bp DNA ROD 05-DEC-1993 ON M. musculus anti-T3 98QQ variable light chain.	ACCESSION KEYWORDS SOURCE	2	immunoglo
KEYWORDS SOURCE ORGANISM	Σ	5010		Eukaryota Metazoa; Vertebrat
			Teti	Tetrapoda
	Vertebrata; Gnathostonary Osteichthyes; Sarcottergrii; Choanata; Tetranda: Ammint: Wammali: Osteichthyes; Sarcottergrii; Choanata; Tetranda: Ammint: Wammali: Dithoris: Dithoris: Didnotti:	REFERENCE		1 (bases
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1111		REFERENCE		unpubilsn 2 (bases
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COMMENT FEATURES	NCBI gi:	וחסר	JOURNAL Sub	Submitted Berdoz, S
nos	rce			des Bover
	/organism="Mus musculus" /sex="femile"	COMMENT FEATURES		NCB1 g1:
	/ell line="kpd" // // // // // // // // // // // // //		source	
V_r	/Bub_clone= 90kW 241.42.32.12 V_region <11.333 /note="light chain"			
BASE COUNT	83 a		exon	
ORIGIN			mRNA 5'UTR	
Query Ma Best Loc Matches	Query Match 78.1%; Score 307; DB 54; Length 333; Best Local Similarity 96.1%; Pred. No. 1.25e-297; Matches 330; Conservative 0; Mismatches 13; Indels 0; Gans 0;		sig_peptide	Φ.
qq	qacattdtqctqacacaqtctcctqcttccttaqctqtatctctqqqqqcaqqqqqcacc 60			
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	61 atctcatqcaqqqccaqcaaaaqtqtcaqtacatctqqctataqttatatqcactqqtac 120		exon	
Qy 12			mat_peptide	υ
Db 121	!1 caacagaaaccaggacagccaccaaactcctcatctatttgcatccaacctagaatct 180		ıntron	
Qy 18		BASE COUNT ORIGIN	COUNT	171

; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; ata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; da; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; :ed (16-NoV-1994) to the EMBL/GenBank/DDBJ databases. J.A. Swiss Institute for Experimental Cancer Research, 155 ch. reresses, 1066 Epalinges, SWITZERLAND
: 673445 J. and Kraehenbuhl, J.P.
c amplification by the polymerase chain reaction of
ged genomic variable regions of immunoglobulin genes from
ybridoma cells /product="variable region of the Ig kappa light chain" 648..690 lobulin; kappa light chain; pseudogene; variable region. tae; mitochondrial eukaryotes; Metazoa/Eumycota group; 17-FEB-1995 nathi; Myomorpha; Muridae; Murinae; Mus. es 1 to 690) ROD us Ig Vkappa-pseudo-HNK20 gene. /cell_type="hybridoma cell" /cell_line="HNK20" ggaggcaccaagctggaaatcaaa 333 195 join (26..65,304..314) /gene="Ig Vkappa-HNK20" join (26..65,304..>647) /gene="Ig Vkappa-HNK20" /organism="Mus musculus" join (1..65, 304..>647) Location/Qualifiers ð DNA 155 dq 069 /rearranged /number=2 a 169 c es 1 to 690) /number=1 304..647 /number=2 /number=1 Submission 315..647 /pseudo 66..303 1..690

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ch 77.9%; Score 306; DB 54; Length 690; 1 Similarity 96.6%; Pred. No. 1.61e-296; 338; Conservative 0; Mismatches 8; Indels 4; Gaps 2;	ttocaggttocactggtgacattgtgctgacacagtctcctgcttccttagctgtatctc 369 	tggggcagagggccaccatctcatacagggccagcaacattgtcagtacatctggctata 429 	gttatatgcactggaaccaacagaaaccaggacagccacccagactcctcatcttg 489 	tatccaacctagaatctggggtccctgccaggtcagtggcagtgggtctgggacagact 549 	tcacctcaacatccatcctgtggaggaggatgctgcaacctattactgtcagcaca 609 	ttagggagc-ttacacgttcggaggggaccaagctggaaataaaa 655 	MUSIGKVR1 706 bp DNA ROD 14-APR-1994 Mouse Ig germline kappa V-region 1.5kb-V-kappa, V-kappa-21E K02159 C-region; V-region; germline; immunoglobulin light chain; immunoglobulin-kappa; immunoglobulin-kappa subgroup vk-21. douse BALB/c embryo DNA, clone GHP53. Muse maculus Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Butheria; Rodentia; Myomorpha; Muridae; Murinae. 1 (Bases 1 to 706) Heinrich, G., Traunecker, A. and Tonegawa, S. Somatic mutration creates diversity in the major group of mouse immunoglobulin kappa-light chains 3. Exp. Med. 159, 417-435 (1984) 84113346 NCBI gi: 197490 Location/Qualifiers 1. 706 Actornism="Mus musculus" Actornism="Musculus" Ac
Query Match Best Local S Matches 33	Db 310 ttc Qy 44 TTC	Db 370 tgg Qy 104 TGC	Db 430 gtt Qy 164 GTJ	Db 490 tat Qy 224 CAT	Db 550 tca Qy 284 TCA	Db 610 tta Qy 344 GTP	RESULT 10 LOCUS P DEFINITION N ACCESSION F KEYWORDS S SEGMENT SOURCE ORGANISM N AUTHORS ITTLE S JOURNAL MEDLINE S COMMENT N FEATURES SOURCE EXON
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DEFINITION	Mouse In light chain V(kanns)218-11(kanns)5 rearranged NNA		
		Qy 284 TCA	TCACCCTCAACATCCATCTGTGGAGGAGGATGCTGCAACCTATTACTGTCAGCACA 34
ACCESSION	XI3938 Y00804 To booms light sheim, In light sheim (semmes)shellin semmining		
NEI WORDS	ig Kappa iight chain; ig iight chain; immunogiobuiin; pseudogene; rearranged NNA; variable region.	659	gragggagcrtcc b4/
SOURCE	house mouse.	Qy 344 GTA	344 GTAGGGAGAATCC 356
ORGANISM	Mus musculus Bukaruotaa: mitochondrial aukaruotas: Matazoa/Ehmuoota aroum:		
	Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;	RESULT 12	
	Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;		MDIGKVBI 333 bp RNA ROD 05-NOV-1994
	Tetrapoda, Amniota, Mammalia, Theria, Eutheria, Glires, Rodentia,	z	M.domesticus IgK variable region.
REFERENCE	octurognatul; myomorpha; muridae; murimae; mur. 1 (bases 1 to 666)	KEYWORDS 3	222098 poti-DNA potihodu. Ink dene, Ink warishle region, immunoalohu
AUTHORS	ą		anti bun antibodi, ign gene, ign variabie region, immunogioba Western European house mouse.
TITLE	Direct Submission	MSIN	Mus musculus domesticus
JOURNAL	- COI		Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
	B., Institut fuer Genetik, Weyertal 121, 5000 Koeln 41, FRG	2	Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chor
REFERENCE	2 (bases 466 to 666)	<i>~</i> 6	Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choan
TITIE	MulletyB. and Ketn,M. Ordered estivation of the Ta lambda locus in Bhelean B sell lines	- <i>u</i>	Tetrapoda; Amniota; Mammaila; Ineria; Eutneria; Gilres; Koden Sciurognathi: Mucmornha: Muridae: Murinae: Mus
JOURNAL	J. Exp. Med. 168 (6), 2131-2137 (1988)	REFERENCE 1	octatognacii, myomorphia, martaae, martiiae, mas. 1 (bases 1 to 333)
MEDLINE	89067821		Tillman, D.M., Jou, N.T., Hill, R.J. and Marion, T.N.
COMMENT	the correctly rearranged V(kappa)21E segment is not functional		Both IgM and IgG anti-DNA antibodies are the products of clon
			selective B cell stimulation in (NZB x NZW)F1 mice
	it carries a 1-bp deletion in the leader sequence Data kindly	JOURNAL J	J. Exp. Med. 1/6 (3), /61-//9 (1992) 02301444
	reviewed (20-NOV-1990) by muchiel b.		22361444 2 (bases 1 to 333)
	NCBI qi: 51649		Marion, T.N.
FEATURES	Location/Qualifiers		Direct Submission
sonrce	1666	AI.	Submitted (23-MAR-1993) to the EMBL/GenBank/DDBJ databases. T
	/organism="Mus musculus"	æi '	Marion, Microbiology and Immunology, University of, Tennessee
	/strain="NH/Swiss"		Memphis, 858 Madison Avenue, Memphis, TN, 38163, USA
	/cell_line="BIP8-/b Abelson 300-19"	COMMENT	NCBI gi: 29/663
misc feature		FEMIUNES	MOCALINI/QUALITIES
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misc_feature			/strain="(NZB x NZW)F1"
4			/dev_stage="somatic_variant"
misc_reature	eacure 04/bb		/tissue_type="spieen" /aall +uaa-"hubridama"
RASE COUNT	160 a 167 c 151 d 188 t		/cell_lype= !!yb!ido#d /cell_lype=#17c 16#
ORIGIN	, , , , , , , , , , , , , , , , , , ,		/isolate="mouse #17"
			/chromosome="6"
Query Match	Query Match 77.1%; Score 303; DB 53; Length 666;	ş	/sex="Female"
Matches	yo.45; zative	cno	✓1>5553 /qene="1qK"
			/note="17s.16 is clonally related to the IgG hybride
95 to 335 to -	335 ttccaqqttccactgqaqacattgtqctqacacaqtctcctqcttccttaqctqtatctc 394		17s.94 and 17s.124 in clone 17s-c4. NCBI gi: 297664
Qy 44 T	TICCAGGITCCACIGGIGACATTGIGGIGACACAGGICTCCTTAGGIGTATCIC 103		
705 tu	nanananananananatan tanan mananananananan at na manananan at ang 15.7		antibody, VK21 tamily" /product="!imminoclobulin pariable region"
			/translation="DIVLTQSPASIAVSLGQRATISCRASQSVSTSAYSYIH
Oy 104 T	GGGGCAGGGGCCACCATGTAGGGGCCAGCAAAAGTGTCAGTACATGTGGGTATA 163		GQTPKLLIKYASNLDSGVPARFSGSGSGTDFTLNIHPVEEEDTATYYCQHSW
Db 455 g	gttatatgcactggtaccaacagaaaccaggacagccacccaaactcctcatctatct	BASE COUNT	88 a 87 c 82 g 75 t 1 others
0v 164 G		ORIGIN	
		Query Match	76.68;
515 dO 	catccaacctagaatctggggtccctgccaggttcagtggcagtgggtctgggacagact 574 	Best Local Matches 3	Best Local Similarity 94.9%; Pred. No. 5.65e-291; Matches 316; Conservative 1; Mismatches 16; Indels 0; Gaps
Qy 224 C	atccaacctagaatctggggtcctggccaggttcagtgggagtgggtctgggacagact 283	יפה 1	naturations on the fort the fortand and the fortand of the fortand
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/translation="DIVLTQSPASLAVSLGQRATISCRASQSVSTSAYSYIHWYQQKP GQTPKLLIKYASNLDSGVPARFSGSGSGTDFTIAIHPVEEDTATYYCQHSWEIPFTF Submitted (23-MAR-1993) to the EMBL/GenBank/DDBJ databases. Tony N. Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; /codon_start=1 /function="kappa light chain variable region for anti-DNA antibody; Vk21 family" Tillman, D.M., Jou, N.T., Hill, R.J. and Marion, T.N.
Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell stimulation in (NZB x NZW)F1 mice
J. Exp. Med. 176 (3), 761-779 (1992) ;**,** anti-DNA antibody; IgK gene; IgK variable region; immunoglobulin. /gene="IgK" /note="178.16 is clonally related to the IgG hybridomas 178.94 and 178.124 in clone 178-c4. NCBI gi: 297664" Marion, Microbiology and Immunology, University of, Tennessee, Memphis, 858 Madison Avenue, Memphis, TN, 38163, USA 05-NOV-1994 Gaps ; Score 301; DB 53; Length 333; Pred. No. 5.65e-291; 1; Mismatches 16; Indels /product="immunoglobulin variable region" 1 others Sciurognathi; Myomorpha; Muridae; Murinae; Mus. ROD /dev_stage="somatic variant" 75 t /organism="Mus domesticus" M.domesticus IgK variable region. /strain=" (NZB x NZW)F1" /tissue_type="spleen" /cell_type="hybridoma" /cell_line="17s.16" /isolate="mouse #17" western European house mouse. Location/Qualifiers b RNA 82 /chromosome="6" Mus musculus domesticus /sex="Female" 333 bp 76.68; 87 c GGGTKLEIK" 1 (bases 1 to 333) (bases 1 to 333) 1 Similarity 94.9%; 316; Conservative Direct Submission <1..>333 1..333 HIIIII III AGGGAGAATCC 356 NCBI gi: 297663 agggagettee 647 Marion, T.N. ø 88 MD I GKVB 1 뜌

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BASE COUNT 85 a 86 c 86 g 75 t 1 others ORIGIN	Query Match 76.3%; Score 300; DB 55; Length 333; Best Local Similarity 94.9%; Pred. No. 7.26e-290; Matches 316; Conservative 0; Mismatches 17; Indels 0; Gaps 0;	Db 1 gacattgtgttgacacagtctcctgcttccttagctgtatcgctggggnagaggccacc 60	Db 61 ctctcatgcagggccaaccaaagtgtcagttcatctggctatagttatatgcactggtac 120	Db 121 caacagaaaccaggacagtcacccaaactctcatcatcaagtatgcatccaacctagaatct 180	Db 181 ggggtccttgccaggttcagtggcagtgggtctgggacagacttcacctcaacatccat 240	Db 241 cctgtggaggagatactgcaacatattactgtcagcacagttgggagattccgttc 300 	Db 301 acgttcggagggggaccaagctggaaataaaa 333 	RESULT 14 LOCUS MMU01973 394 bp mRNA ROD 24-SEP-1993 DEFINITION Mus musculus Balb/c anti-CD18 Ig light chain variable region mRNA, partial cds.	ACCESSION U01973 KEYWORDS SOURCE mouse ORGANISM Mus musculus	Eucaryotae; Marazoa; Chordata; Vertebrata; Gnathostomata; Mammalla; Eutheria; Rodentia; Myomorpha; Muridae; Mus. REFERENCE 1 (bases 1 to 394) AITHORS Heiso K Rajnrath 1 and Harris 1.1	TITLE Humanization of 60.3, an anti-CD18 antibody JUNNAL Unpublished REFERENCE 2 (bases I to 394) AUTHORS Harris.L.J.		Avenue, Seattle, WA 98121 USA COMMENT NCBI gi: 403071 FEATURES Location/Qualifiers source 1394	/organism="Mus musculus" /oell_line="60.3 hybridoma" /cell_type="hybridoma" (B-cell)" /tiono the properties of the pro	/ Lissue_Lype= spien / dee_stage="adult" i60 / note="nucleotides 1-29 derived from PCR primer and may not reflect mRNA sequence"
Qy 61 GACATTGTGCTGACAGTCTCCTTGGTGTATCTCTGGGGCAGAGGGCCACC 120	61 atotoatgoaggocaacaaagtgtoagyacatctgoctatagttatattcactggtac 	121 caacagaaaccaggacagacaccaaactcctcatcaagtatgcatccaacctagattct 	181 ggggtcctgccaggttcagtggcagtgggtctgggacagacttcacctcaacatccat		Db 301 acgttcggagggggaccaaactggaaataaaa 333 	RESULT 13 LOCUS MMVL103 333 bp RNA ROD 05-AUG-1995 DEFINITION Mouse mRNA for kappa-immunoglobulin light chain V-J region (cell		ORGANISM Mus musculus Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Osteichthyes; Sarcopterygii; Mammalia; Eutheria; Rodentia; Sciurognathi; Myomorpha; Murinae; Mus. REFERENCE I (bases I to 333)	Rei Dir Sub Rei	rue michel servet, th-1211 teneve 4, SWitzerland REFERENCE 2 (bases 1 to 333) AUTHORS Reininger, L., Shibata, T., Ozaki, S., Shirai, T., Jaton, J.C. and Trui, S.	TITLE Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies from autoimmune NZB mice JOURNAL Eur. J. Immunol. 20 (4), 771-777 (1990) MEDLINE 90269328	93		/_regroun	/codour_statc=1 /product="kappa-1g light chain (111 AA)" /translation="DIVUTQSPASIAVSLGXRATLSCRASQSVSSGSYSYMHWYQQXP /translation="DIVUTQSPASIAVSLGXRATLSCRASQSVSSGSSSSYSYMHWYQQXP GQSPKILIKYASNLESCVPARFSGSGSGTDFTLAIHPVEEEDTATYYCQHSWEIPFTF GGGTKLEIK"

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A 4 nt deletion at the V-J recombination site causes misalignment of the V and J segments resulting in a nonfunctional kappa-chain. Immunoglobulin transcripts and molecular history of a hybridoma that produces antibody to carcinoembryonic antigen 30-JUN-1987 Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; MUSIGKAAS 339 bp mRNA ROD 30-JUN-19 Mouse immunoglobulin aberrantly rearranged kappa-chain mRNA Length 339; C-region; J-region; V-region; immunoglobulin-kappa; processed gene; pseudogene. Mouse hybridoma CEA 66-E3, cDNA to mRNA. Eutheria; Rodentia; Myomorpha; Muridae; Murinae. pept V138J2-region from hybridoma CEA 66-E3 /note="pseudo-IgK precursor" 76 t 361 ACCTTCGGAGGGGGACCAACTGAAA 393 /note="pseudo-IgK leader organism="Mus musculus"

Qy 295 ATCCATCCTGTGGAGGAGGAGGATGCTGCAACCTATTACTGTCAGCACAGTAGGGAGAAT 354 Jul 8 08:22

Search completed: Mon Jul 8 08:33:17 1996 Job time: 351 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch nn

MasPar time 182.60 Seconds 773.735 Million cell updates/sec Mon Jul 8 08:34:42 1996; Run on:

not generated. Tabular output

>US-08-137-117B-24 (1-393) from USO8137117B.seq 393 Title:

Description: Perfect Score:

1 ATGGAGTCAGACACTCCT......GGACCAAGCTGGAATAAAA 393 TACCTCAGTCTGTGAGGA.......CCTGGTTCGACCTTTATTT N.A. Sequence:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0

STD:

Nmatch

518261 seqs, 179750453 bases x 2 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

EST-STS

1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8 9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14 11:EST19 10:EST19 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14 11:EST12 12:EST21 21:EST21 22:EST22 23:EST23 24:EST23 24:EST23 26:EST26 27:EST23 23:EST23 24:EST23 24:EST23 23:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST36 33:EST33 34:EST34 35:EST35 36:EST44 43:EST44 44:EST44 44:EST44 44:EST44 45:EST45 66:EST66 67:EST66 67:EST66 67:EST66 67:EST66 67:EST66 67:EST66 67:EST66 67:EST67 67:EST68 67:EST68 67:EST68 67:EST68 67:EST79 77:EST77 77:EST78 77:

EST-STS-TWO

Database:

100:gnEST6 101:gnEST7 102:gnEST8 103:gnEST9 104:gnEST10 105:gnEST11 106:gnSTS1 107:gnSTS2 108:gnSTS3 109:enEST1 100:gnEST2 111:enEST3 112:enEST4 113:enEST5 114:enEST6 115:enEST7 115:enEST7 115:enEST7 115:enEST1 115:enEST1 115:enEST1 115:enEST1 120:enEST1 120:enEST1 121:enEST13 122:enEST14 123:enEST15 124:enEST15 125:enEST17 126:enEST18 127:enEST19 95:gnEST1 96:gnEST2 97:gnEST3 98:gnEST4 99:gnEST5

Jul 8 08:27

128:enEST20 129:enEST21 130:enSTS1 131:enSTS2 132:enSTS3

US-08-137-117B-24.rst

Variance 1.898; scale 5.268 Mean 10.000;

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	a 4.04e-1	.74e-16	1 2.06e-	2.06e - 15	9.43e - 1	9.43e - 13	e u	1.05e-13	1.50e-12	1.50e-1	1.72	1.83e-1	1.83e-11	1.83e-1	a 1.83e-1	1.93e - 11	~	· ·	7	7	CO.	~	۲;		Ø		a	je.	e 2.22e-1	0 C	2.036-0	3 2.03e-	2.03e-9	e 1.58e-	a 1.44e-8	e 1.44e-8	e 1.17e-8	e 1.17e-8	e 1.03e-	e 8.98e-7	7.74e-	7.74e-7	
	Description	Ното в	5d05.rl Homo s	Г100049 Ношо в	9 Ното ва	.rl Homo	Ношо в	175 Homo s	EST100475 Homo sapien	EST69270 Homo sapiens	0 Нопо		0 Home	Ношо 8	6.rl Hc	rl Homo s	rl Hom	Ното в	11 Home	j82d09.rl Homo	8	EST19007 Homo sapiene	j83c03.rl Homo	CO.	3 Ношс	EST77181 Homo sapien	ST77181 Homo	1 Homo	4.rl Homo	ri Homo s	yez4eU/.rl Homo sapie	Homo s	EST89211 Homo s	.rl Homo	161q07.rl Homo s	rl Homo s	rl Homo s	rl Homo s	j55c03.rl Homo a	j54h03.rl Homo	j81d08.rl Homo	i85f01.r1 Hom	Homo 8	
	110	H25625		12	6	HS115213		2	T27587	T29104	HS10412	R48141	HS11411	_	HS156227	н69156	R28232	916	HS91615	R69532	T27870	HST27870	R69482		HST27593	HS34210	T29342	- :	HS841242	K64693	195176 H39743	T29656	55	R67559	H27642	33	23	1	R49771	2	029	990	Ξ	
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	Score	123	105	104	0	93	83	95	92	88	88	98	82	82	82	82	84	83	83	83	82	85	11	11	11	16	76	76	76	6 H	3 5	3.5	73	73	69	89	89	99	99	65	64	63	63	,
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	EST 10-JUL
	mRNA
	488 bp
-	H25625
RESULT	LOCUS

DEFINITION

ACCESSION

KEYWORDS

SOURCE

Homo sapiens

ORGANISM

REFERENCE AUTHORS Wilson, R.

JOURNAL

US-08-137-117B-24 rat

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FEATURES

Best Local Similarity

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EST 06-SEP-1995 EST100049 Homo sapiens cDNA 5' end similar to immunoglobulin light chain, V region (HT:3078). Eutheria; Archonta; Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 364)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldher, R.A.,
Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W.,
Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr, P.S., 9 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; 205 203 agctgctcatttactgggnatctacccggggaatccgggggtccctgaccgattcagtggca 262 263 gcgggtctngggacanatttcantctcaacctcagcggnctgcaggttgaagatgtggca 322 92 TAGGIGIAICTCTGGGGCAGAGGGCCACCATCTCATGCAGGGCCAGCAAAAGTGTCAGT- 150 143 acagetecaacaatacgaaetacttagettggtaccaaetgaaaccaggacageeteeta 202 206 AACTCCTCATCTATCTTGCATCCAACCTAGAATCTGGGGTCCCTGCCAGGTTCAGTGGCA 265 83 266 GTGGGTCT-GGGACAGACTTCACCCTCAACATCCATCCTGTGGAGGAGGATGCTGCA 324 2 Gaps Contact: Venter, JC The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878 Tel: 3018699056 Fax: 3018699423 Email: tdbinfo@tdb.tigr.org For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org). NCBI gi: 609677 tgttgctctggatctctggtgcctacggggacaccgtgatgacccagtctccagactccc 32 TGCTGCTCTGGGTTCCAGGTTCCACGTGCTGCTGCTGCTGCTGCTGCTTCCT 7; Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Length 364; cDNA Sequence"; "Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence" Indels human primer=M13 Reverse library=Human Pancreas. Sequence 364 BP; 80 A; 98 C; 87 G; 93 T; 6 other; 0; Mismatches 94; 26.5%; Score 104; DB 127; 70.0%; Pred. No. 2.06e-158; 323 gtttattactgtcagcaatattattatactccgtaca 359 325 ACCTATTACTGTCAGCACAGTAGGGAGAATCCGTACA 361 /organism="Homo sapiens" Location/Qualifiers /note="human" 236; Conservative <1..>364 1..364 Homo sapiens Local Similarity Unpublished Query Match source DEFINITION ORGANISM Matches 23 ACCESSION KEYWORDS

AUTHORS

US-08-137-117B-24 rat

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yu40h01.r1 Homo sapiens cDNA clone 236305 5' similar to gb:X72431 IG KAPPA CHAIN V-II REGION (HUMAN); clone=236305 primer=M13RP1 library=Soares ovary tumor NbHOT vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) Rsitel=Not I Rsite2=Eco RI Female. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' 166 TATATGCACTGGTACCAACAGAAACCAGGACAGACACCCAAACTCCTCATCTTGCA 225 79 tectategggeetetgeagteceagaeaggtteagtggeagtgggteaggeaetgattte 138 226 TCCAACCTAGAATCTGGGGTCCCTGCCAGGTTCAGTGGCAGTGGGGTCTGGGACAGACTTC 285 286 ACCCTCAACAICCAICCIGIGGAGGAGGAGGAIGCIGCAACCIAITACIGICAGCACAGI 345 19 tattingactggtacctgcagaagccagggcagtctccacagctcctgatctatacgctt 78 06-0CT-1995 Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R., est@watson.wustl.edu High quality sequence stops: 354 Source: IMAGE Consortium, LINL This clone is available royalty-free through LINL Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: yu40h01.r1 Homo sapiens cDNA clone 236305 5' similar to gb:X72431 contact the IMAGE Consortium (info@image.llnl.gov) for further ; 0 Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae Score 93; DB 114; Length 470; Pred. No. 9.43e-136; 199 atagagtttccttggacttttggccaggggaccaagctggagatcaaa 246 Indels Sequence 470 BP; 112 A; 108 C; 119 G; 120 T; 11 other; 0; Mismatches 68; 08-OCT-1995 (Rel. 45, Created) 08-OCT-1995 (Rel. 45, Last updated, Version 1) /organism="Homo sapiens" G KAPPA CHAIN V-II REGION (HUMAN); mRNA Location/Qualifiers standard; RNA; EST; 470 /clone="236305" "The WashU-Merck EST Project"; information. NCBI gi: 1014947 470 bp 23.7%; 160; Conservative <1..>470 Homo sapiens (human) Local Similarity H62115 H62115 EST. Unpublished HS115213 Query Match ٠ source DEFINITION mRNA Matches ACCESSION KEYWORDS RESULT S 음 ð g ð 엄 δ 유 δ

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A Kelley J.M., Klimek K.M., Kelley J.C., Liu L.I., Marmaros S.M., Merrick J.M., Klimek K.M., Kelley J.C., Liu L.I., Marmaros S.M., Merrick J.M., NORENO-PALANQUES R.F., McDonald L.A., Nguyen D.T., Pellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L., Marmaros S.M., A Saudek D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R., Meidman J.E., Li Y., Bednarik D.P., Cao L., Cepeda M.A., Fischer C., Hastings G.A., He W.W., Hu J.S., Greene J.M., Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li H., Meisner P.S., Olsen H., Raymond L., Wei Y.F., Wing J., Xu C., Yu G.L., Ruben S.W., Dillon P.J., Fannon M.R., Rosen C.A., M. Haseltine W.A., Fields C., Fraser C.M., Venter J.C.; Traser C.M., Venter J.C.; Traser C.M., Venter J.C.; Patterns Based Upon 52 Million Basepairs of cDNA Sequence"; 85 tetecaetetecetgeceginaceetggagageceggeetttateteetgeaggtetagt 144 79 TCTCCTGCTTCCTTAGGTGTATCTCTGGGGCGAGGGGCCACCATCTCATGCAGGGCCAGC 138 145 cagagactcctgcatagtactggacacaactatttggattggtacctgcagaagccaggg 204 cagtetecacaacteetgatetatttgggttetaategggeeteegggggteetgaeagg 264 196 CAGACACCCAAACTCCTCATCTTGCATCCAACCTAGAATCTGGGGTCCCTGCCAGG 255 265 ttcagtggcagtgggatcaggcacagattttacactgaaaataagcagagtggaggctga 324 19 CTGCTATGGGTACTGCTGTGGTTCCAGGTTCCACTGGTGACATTGTGCTGACACAG 78 84 Gaps and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org). NCBI gi: 609685 Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A., Bult C.J., 1ee N., Kirkness E.F., Weinstock K.G., Gocayne J.D., White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.W., Clayton R.L., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D., FitzGerald L.M., FitzHugh W.M., Fritchman J.L., Geoghagen N.S.M., Glodek A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle Jr P.S., Contact: Venter, JC The Institute for Genomic Research 932 Clopper ctcctggggctgctaatgctctgggtctctggatccagtggggatattgtnctgactcag EST100475 Homo sapiens cDNA 5' end similar to immunoglobulin kappa Rd, Gaithersburg, MD 20878 Tel: 3018699056 Fax: 3018699423 Email: tdbinfoetdb.tigr.org For clone availability, additional sequence 4; Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae Score 92; DB 127; Length 359; 0; Mismatches 93; Indels Sequence 359 BP; 75 A; 93 C; 95 G; 94 T; 2 other; Pred. No. 1.05e-133; (Rel. 42, Created) (Rel. 45, Last updated, Version 2) light chain V region (GB:X63397) (HT:3865) /organism="Homo sapiens" Location/Qualifiers /note="human" 23.4%; 68.1%; I 207; Conservative <1..>359 Homo sapiens (human) Local Similarity 07-SEP-1995 Unpublished Query Match source Matches 25 202 mRNA Best] 유 δ d δ 임 δ g ð 셤

4;

double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; ö This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. 79 tcctatcgggcctctgcagtcccagacaggttcagtggcagtgggtcaggcactgatttc 138 286 ACCCTCAACATCCATCCTGTGGAGGAGGAGGATGCTGCAACCTATTACTGTCAGCACACAT 345 226 TCCAACCTAGAATCTGGGGTCCCTGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTC 285 19 tattingaciggiaccigcagaagccagggcagictccacagciccigaictatacgcii 78 Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 470)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rikkin, L., Rohlfing, T., Soaree, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Gaps Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 ; 0 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Score 93; DB 97; Length 470; 199 atagagtttccttggacttttggccaggggaccaagctggagatcaaa 246 11 others 346 AGGGAGAATCCGTACACGTTCGGAGGGGGGGACCAAGCTGGAAATAAAA 393 0; Mismatches 68; Indels US-08-137-117B-24.rst Pred. No. 9.43e-136; 120 t /organism="Homo sapiens" High quality sequence stops: 354 Source: IMAGE Consortium, LLNL HST27587 standard; RNA; EST; 359 BP T27587; 119 g Location/Qualifiers Email: est@watson.wustl.edu The WashU-Merck EST Project /clone="236305" WashU-Merck EST Project Query Match 23.7%; Best Local Similarity 70.2%; 108 c 160; Conservative Contact: Wilson RK Unpublished (1995) <1..>470 NCBI gi: 1014947 Homo sapiens æ Wilson, R. 112 source ORGANISM BASE COUNT Matches REFERENCE AUTHORS FEATURES RESULT ORIGIN E S 임 셤 g ð g ò ò à

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Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldher, R.A.,
Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
Rhite, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W.,
Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M.,
Glodek, A., Ghehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr.P.S.,
Merick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T.,
Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Soctt, J.L.,
Saudek, D.M., Shirley, R., Saall, K.V., Spriggs, T.A., Utterback, T.R.,
Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A.,
Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A.,
Fischer, C., Hastings, G.A., He, M.-W., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C. Initial Assessment of Human Gene Diversity and Expression Patterns T29104 357 bp mRNA EST 06-SEP-1995 EST69270 Homo sapiens CDNA 5' end similar to immunoglobulin kappa Deuterostomia, Chordata, Vertebrata, Gnathostomata, Osteichthyes, Sarcopterygii, Choanata, Tetrapoda, Amniota, Mammalia, Theria, Eutheria, Archonta, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 357) 196 CAGACACCCAAACTCCTCATCTATCTTGCATCCAACCTAGAATCTGGGGTCCCTGCCAGG 255 85 tetecaetetecetgeceginacecetggagageeggeetitatetectgeaggietagi 144 205 cagtetecacaactectgatetatttgggttetaategggeeteeggggteeetgaeagg 264 human primer=M13 Reverse library=Human Lymphoid tissue. Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Based Upon 52 Million Basepairs of cDNA Sequence Unpublished (1995) light chain V region (GB:X54248) (HT:3095). T29104 Contact: Venter, JC The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878 Tel: 3018699056 Other_ESTs: EST69269 Homo sapiens ||||| |GGAT 318 ggat 328 VITION CE GANISM URNAL 325 315 SSION RENCE RDS E

US-08-137-117B-24 rst

Email: tdbinfoëtdb.tigr.org For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database ä 95 intecactetecetyceegteaceetygaagageeggtetecatetectgeaggtetagt 154 274 255 334 155 cagagectectacatactaatggatacatetatttggattggtacetgeagaagecaggg 214 ctcctggggctgctaatgctctgggtctctggntccagtggggatattgtgatgactcag 94 Gaps Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A., Bult C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D., White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.W., Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Filz Hugh W.M., Fritchman J.L., Geoghagen N.S.M., Clodek A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle Jr P.S., Kelley J.M., Klimek K.M., Kelley J.C., Liu L.I., Marmaros S.M., 275 ttcagtggcagtatttcaggcacagattttacactgaaaatcaagcagagtggaggttaa 215 cagtctncacaactcctgatctctttgggttctaatcgggcctccggggtccctgacagg EST69270 Homo sapiens cDNA 5' end similar to immunoglobulin kappa light chain V region (GB:X54248) (HT:3095). 4; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Length 357; 3 others 0; Mismatches 96; Indels Pred. No. 1.50e-125; 09-JAN-1995 (Rel. 42, Created) 08-SEP-1995 (Rel. 45, Last updated, Version 2) EST69270 Homo sapiens cDNA 5' end similar to in Score 88; DB 70; 99 /organism="Homo sapiens" /note="human" standard; RNA; EST; 357 BP Location/Qualifiers 6 8 (tdbinfo@tdb.tigr.org) Query Match 22.4%; Best Local Similarity 67.2%; Matches 205; Conservative 93 c <1..>357 1..357 NCBI gi: 611202 Homo sapiens (human) 72 335 ggatg 339 GGATG 319 HS10412 T29104; source 1-357 BASE COUNT 35 13 315 FEATURES ORIGIN g g දු 셤 원 ò δ à ð ð ò

A Merrick J.M., MORENO-PALANGUES R.F., McDonald L.A., Nguyen D.T.,
Rellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L.,
Saudek D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R.,
M. Gidman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A.,
A. Coleman T.A., Collins E.J., Dimke D., Feng P., Ferrie A.,
Fischer C., Hastings G.A., He W.M., Hu J.S., Greene J.M.,
A. Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li H.,
A. Maisener P.S., Olsen H., Raymond L., Wei Y.F., Wing J., Xu C.,
A. Yu G.L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A.,
A. Haseltine W.A., Fields C., Fraser C.M., Venter J.C.,
I'mitial Assessment of Human Gene Diversity and Expression
Retterns Baseed Upon 52 Million Basepairs of CDNA Sequence", Other ESTE: EST69269 Contact: Venter, JC The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878 Tel: 3018699056 Fax: 3018699423 Email: tdbinfo@tdb.tigr.org For clone availability, additional sequence and expression information related to this EST, Li H., please contact the TIGR Database (tdbinfo@tdb.tigr.org). NCBI gi: Location/Qualifiers Unpublished.

4; Score 88; DB 114; Length 357; Pred. No. 1.50e-125; 0; Mismatches 96; Indels Sequence 357 BP; 72 A; 93 C; 90 G; 99 T; 3 other; 22.4%; Best Local Similarity 67.2%; Query Match Matches

/organism="Homo sapiens"

source

/note="human"

ä 94 Gaps 35 ctcctggggctgctaatgctctgggtctctggntccagtggggatattgtgatgactcag 205; Conservative 유 ð 음 ð

274 196 CAGACACCCAAACTCCTCATCTTGCATCCAACCTAGAATCTGGGGTCCCTGCCAGG 255 155 cagagcetectacatactaatggatacatetatttggattggtacetgcagaagecaggg 214 139 AAAAGTGTC--AG-TACATCTGGCTATAGTTATAGCACTGGTACCAACAGAAACCAGGA 195 ttcagtggcagtatttcaggcacagattttacactgaaaatcaagcagagtggaggttaa 334 cagtetneacaactectgatetetttgggttetaategggeeteeggggteeetgaeagg __ = = = = -215 275 g ð 쇰 ð 셤 δ

R48141 445 bp mRNA EST 18-MAY-1995 yj66c09.rl Homo sapiens cDNA clone 153712 5' similar to gb:X72467 human clone=153712 library=Soares breast 2NbHBst vector=pT7T3D IG KAPPA CHAIN PRECURSOR V-II REGION (HUMAN); contains Alu 445 bp repetitive element;. 315 GGATG 319 R48141 EST. RESULT 11 DEFINITION ACCESSION KEYWORDS SOURCE à

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234 AGAATCTGGGGTCCCTGCCAGGTTCAGTGGCTGTGGGTCTGGGACAGACTTCACCCTCAA 293 g à g 셤 g δ ð modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 230. Library constructed by Bento Soares and M.Fatima Bonaldo. digested with Not I and cloned into the Not I and Eco RI sites of Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; 4; resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI Adult female. double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), This clone is available royalty-free through LLNL; contact the MAGE Consortium (info@image.llnl.gov) for further information. 139 cagagcetectgtatectaatggttaceactatttggattggtacetecagaagecaggg 198 79 tetecactetecetgecegteaceetggagagegeetecatetectgeaggtetagt 138 139 AAAAGTGTCA-GTA-CATC-TGGCTATAGTTATATGCACTGGTACCAACAGAAACCAGGA 195 cagtetecacagetecteatetatttgggttetaategggeeteeggggteeetgacagg 258 (Pharmacia) with a modified polylinker host=DH10B (ampicillin Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Iennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Gaps Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 4; Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Query Match 21.9%; Score 86; DB 47; Length 445; Best Local Similarity 69.2%; Pred. No. 1.72e-121; 8 others 0; Mismatches 81; Indels Washington University School of Medicine ų 120 /organism="Homo sapiens" High quality sequence stops: 302 Source: IMAGE Consortium, LLNL 119 g Location/Qualifiers Email: est@watson.wustl.edu The WashU-Merck EST Project /clone="153712" WashU-Merck EST Project /note="human" 115 c (bases 1 to 445) 191; Conservative Contact: Wilson RK Unpublished (1995) Tel: 314 286 1800 Fax: 314 286 1810 1..445 NCBI gi: 810167 Homo sapiens ส Wilson, R. source BASE COUNT ORIGIN Matches ORGANISM TITLE JOURNAL 199 196 REFERENCE AUTHORS FEATURES

Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A.,
Bult C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D.,
White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.W.,
Clayton R.A., Cline R.T., Cotton M.D., Earle-Hudhes J., Fine L.D.,
Ricagrand L.M., Firthudh W.M., Fritchman J.L., Geoghagen N.S.M.,
Glodek A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle Jr P.S.,
Relley J.M., Klimek K.M., Kelley J.C., Liu L.I., Marmaros S.M.,
Merick J.M., MORENO-PALANQUES R.F., McDonald L.A., Nguyen D.T.,
Relley J.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R.,
Reidman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A.,
Reidman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A.,
Reidman J.F., Li Y., Bednarik D.P., Gao L., Cepeda M.A.,
Rudek D.M., Shirley R., Small K.W., Hu J.S., Greene J.M.,
Ruder J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li H.,
Meissner P.S., Olsen H., Raymond L., Wei Y.F., Wing J., Xu C.,
Rudellin W.A., Fielda G., Fraser C.M., Venter J.C.,
Raseltine W.A., Fielda G., Fraser C.M., Venter J.C.,
Ruttial Assessment of Human Gene Diversity and Expression 232 ggccgctggcatcccagacagdttcactggcagtgggtctgggacagacttcactctcac 291 172 ctggtaccagcagaaacctggccaggctcccaggctcctcatctatgatgcatccaacag 231 Gaps Contact: Venter, JC The Institute for Genomic Research 932 Clopper and expression information related to this EST, please contact the Rd, Gaithersburg, MD 20878 Tel: 3018699056 Fax: 3018699423 Email: EST69430 Homo sapiens cDNA 5' end similar to immunoglobulin light chain V(III),J(V) regions (GB:227170) (HT:3121). tdbinfo@tdb.tigr.org For clone availability, additional sequence ä Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae. 21.6%; Score 85; DB 114; Length 381; Indels IIGR Database (tdbinfo@tdb.tigr.org). NCBI gi: 611212 = = = = = Sequence 381 BP; 86 A; 109 C; 97 G; 86 T; 3 other; 0; Mismatches 39; Best Local Similarity 76.3%; Pred. No. 1.83e-119; 09-JAN-1995 (Rel. 42, Created) 08-SEP-1995 (Rel. 45, Last updated, Version 2) EST69430 Homo sapiens cDNA 5' end similar to in 256 TTCAGTGG-CAGTGGGTCTGGGACTTCACCCT 290 259 ttcagtgggcagtggttcaggcacagattttacact 294 /organism="Homo sapiens' Location/Qualifiers standard; RNA; EST; 381 /note="human" 129; Conservative Homo sapiens (human) Unpublished Query Match HS11411 T29114; source 1 - 381Matches

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292 catcagcagacttggagcctgaagattttgcagtgtattnctgtcagca 340

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T29114 EST.

ACCESSION

KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

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DEFINITION

Jul 8 08:27

US-08-137-117B-24 rat

JOURNAL

COMMENT

TITLE

Query Match

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FEATURES

÷ 144 caaagoctcgtacacagtgatgaaacacctacttgagttggcttcagcagaggccaggc 203 84 actocactotoctoacotytoaccottggacagooggoctocatotoctgcaggtotagt 143 139 AAAAGTGTCAGT-ACA-TC-TGGCTATAGTTATATGCACTGGTACCAACAGAAACCAGGA 195 204 cagcetecaagaetectaatttataagatttetaaceggttetetggggteecagaeaga 263 234 AGAATCTGGGGTCCTGCCAGGTTCAGTGGCAGTGGGTTCAGGACTTCACCTCAA 293 24 cttctggggctgctaatgctctgggtccctggatccagtggggatattgtgatgacccag 83 Gaps estewatson.wnstl.edu High quality sequence stops: 267 Source: IMAGE Consortium, LINL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.; "The WashU-Merck EST Project"; School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: Contact: Wilson RK WashU-Merck EST Project Washington University 3; Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae. Score 85; DB 115; Length 430; Pred. No. 1.83e-119; 0; Mismatches 85; Indels 292 catcagcagacttggagcctgaagattttgcagtgtattnctgtcagca 340 294 CATCCATCCTGT-GGAGGAGGAGGATGCTGCAACCTATTACTGTCAGCA 341 yr86f06.rl Homo sapiens cDNA clone 212195 5' similar to Sequence 430 BP; 98 A; 107 C; 116 G; 101 T; 8 other; qb:X55400 cdsl IG KAPPA CHAIN PRECURSOR V-II REGION 21-0CT-1995 (Rel. 45, Created) 21-0CT-1995 (Rel. 45, Last updated, Version 1) = = =

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Gaps

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Score 85; DB 98; Length 430; Pred. No. 1.83e-119;

Query Match 21.6%; Best Local Similarity 68.0%;

187; Conservative

Matches

0; Mismatches 85; Indels

Jul 8 08:27 US-08-137-117B-24 rat

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144 caaagcctcgtacacagtgatggaaacacctacttgagttggcttcagcagaggccaggc 203 196 CAGACACCCAAACTCCTCATCTATCTTGCATCCAACCTAGAATCTGGGGTCCCTGCCAGG 255 84 actocactetecteacetgteacettggacageeggeetecatetectgeaggtetagt 143 83 19 CTGCTATGGGTACTGCTCTGGGTTCCAGGTTCCACGTGACATTGTGCTGACACA 78 cttctgggggctgctaatgctctgggtccctggatccagtggggatattgtgatgacccag = = = = 264 ttcagtggcagtngggcagggacagatttcacact 298 256 TTCAGTGGCAGTGGGTCTGGGACAGACTTCACCCT 290 염 Op g g 음 δ ð ò ă δ

Search completed: Mon Jul 8 08:38:06 1996 Job time: 204 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Mon Jul 8 08:28:23 1996, MasPar time 7.40 Seconds 447.403 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-137-117B-25 (1-131) from US08137117B.pep 942 Description: Perfect Score:

1 MESDTLLLMVLLLWVPGSTG......CQHSRENPYTFGGGTKLEIK 131 Sequence:

PAM 150 Gap 11 Scoring table:

82306 seqs, 25270970 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4 8:unann5 9:unann6 10:unann7 11:unann8 12:unrev1 13:unrev2

Mean 41.173; Variance 148.737; scale 0.277 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Г	_	7										
	Pred. No.	2.53e-81	8.54e-79	9.95e-77	3.08e-75	4.01e-75	7.84e-73	2.76e-69	8.41e-68	5.30e-67	5,63e-66	2.09e-65	1.310-64
	Description	immunoglobulin light	Iq kappa chain precu	Iq kappa chain precu	Ig kappa chain precu	Ig kappa chain precu	aberrant kappa trans	Ig kappa chain V reg	Iq kappa chain V reg	Ig kappa chain V reg	Iq kappa chain V req	Ig kappa chain V reg	antigen-Fab VI Pae
	QI	555027	PN0446	KVMSM6	KVMS32	PH1226	JL0073	\$52448	KVMS84	KVMS75	KVMS40	KVMS85	545715
	DB	13	S	7	7	S	13	11	7	7	7	7	1
	Query Match Length DB	131	140	131	132	131 5	128	128	111	111	111	111	112
*	Query Match	91.2	88.9	86.9	85.6	85.5	83.3	80.0	78.7	77.9	77.0	76.4	75.7
	Score	859	837	819	908	802	785	754	741	734	725	720	713
	Result No.	1	7	m	4	2	9	7	œ	6	10	11	12

.33e-64	81e-	05e-	3.97e-63	.62e-61	.62e-61	.76e-60	.65e-60	.02e-59	.72e-59	.76e-59	.76e-59	.07e-58	.39e-58	. 95e-58	.12e-57	.12e-57	.46e-57	.45e-57	.32e-56	. 23e-55	.,59e-55	.06e-55	06e-55	.51e-55	.66e-54	.69e-54	.08e-5			-1	0e-	39e-51
chain p	V-J r	kappa chain V reg 3	chain precu	kappa chain V reg 2	kappa chain V reg 2	chain V	chain V	chain V	kappa chain V reg 1	kappa chain V reg 3	chain V	kappa chain V reg 1	chain V	kappa chain V reg 3	kappa chain V reg 1	chain V	chain V	kappa chain V reg 2	light chain V reg 4	kappa chain V reg 1	kappa chain V-J r 1	i-glycoprotein H 2	kappa chain V reg 2		kappa chain V reg 1	kappa chain V reg 4	chain V	kappa chain V-J r 1	kappa chain V reg 2	l antibo	Ξ.	light chain VJ r 2
, ,			S06732 1g	KVMSC1 19	S19972 Ig	KVMS43 Ig		S19976 Ig	KVMS08 Ig	KVMS54 Ig	PH0092 Ig	KVMS37 Ig	_			S19973 Ig	PL0081 Ig					D45722 ant	KVMS80 Ig	Н	Н	S37202 Ig	H	Н	Н		_	S38807 IgG
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- 1	74.6	7							70.9							69.5							67.	99	99	65.8	65.	65.		64.		63.
13 707	14 703	15 701	16 700		18 684	19 675	20 673	21 670				25 661		27 656			30 651		32 638	33 634		_	36 632		_	39 620				43 603	44 599	45 596

ALI GNMENTS

	\$55027 #type complete	immunoglobulin light chain variable region precursor - mouse	(fragment)	#formal name Mus musculus #common_name house mouse	23-Aug-1995 #sequence_revision 23-Aug-1995 #text_change	23-Aug-1995	ONS S55027	JE S55027	nors Jeffrey, P.D.; Schildbach, J.F.; Chang, C.Y.; Kussie, P.H.;	Margolies, M.N.; Sheriff, S.	J.	le Structure and specificity of the anti-digoxin antibody 40-50.		#status preliminary	fresidues 1-131 ##label JEF	##cross-references EMBL:L31404	#length 131 #molecular-weight 14243 #checksum 6089	Match 91.2%; Score 859; DB 13; Length 131;	Similarity 91.68;	120; Conservative	1 motedell limit 1 limmand and int to mand and amount incomed another to		1 MESDILLIAVILLAVIGOROPASIGOIVLTOSPASIGOSATISCRASKSVSTSGYSYMHWY 60
RESULT 1	ENTRY	TITLE		ORGANISM	DATE		ACCESSIONS	REFERENCE	#authors		# journal	#title	#accession	##status	##residues	##cross-r	SUMMARY	Ouerv Match	Best Local Si	Matches 120	10 to to to	1	Ov 1 MESDT

61 qqkpqqppklliylasilesgvparfsgsgsgtdftlnihpveeedaatyycqhsreypl 120 	21 tfgagtelelk 13 	PN0446 #type fragment Ig kappa chain precursor V-II region - human (fragment) #formal name Homo sapiens #common_name man 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Apr-1995 PN0446 PN0446	thois natura, b.; betil, b.; blandintbeth, l.; methie, U.H. U.H. Gene (1992) 122:321-328 tle A general method for chimerization of monoclonal antibodies by inverse polymerase chain reaction which conserves authority N-terminal sequences.	PN le_ty es refer #s	#domain signal sequence #status predicted #label 516\ 140 #product Ig light chain kappa-2 V region #status predicted #label MAT Y #length 140 #checksum 3597	y Match 88.9%; Score 837; DB 5; Length 140; Local Similarity 91.6%; Pred. No. 8.54e-79; hes 120; Conservative 3; Mismatches 6; Indels 2; Gaps 1;	<pre>1 metdtlllwvplgtgdivltgspaslav8jggratisyrasksvstsgysymhwn 60 1{: </pre>	61 qqkpqpprlliylvsnlesgyparfsqsgsgtdftlnihpveeedaatyycqhire1 118 	119 tfgggtkleik 129 21 TFGGGTKLEIK 131	XVMSM6 #type complete Ig kappa chain precursor V regions (M63, AB22, PC9245,		Al-bec-1993 B90412; B90314; B93822; C93204; D93204; A01935 ERENCE A90412. Burstein, Y.; Schechter, I. #journal Biochemistry (1978) 17:2392-2400 #title Primary structures of N-terminal extra peptide segments
Db 61 Qy 61	Db 121 Qy 121	RESULT 2 ENTRY TITLE ORGANISM DATE ACCESSIONS REFERENCE A	#authols #journal #title	#accesion ##molecu ##residu ##cross- CLASSIFICATION KEYWORDS	1-20 21-140 SUMMARY	Query M Best Lo Matches	9b 0y	Db 61 Qy 61	Db 119	RESULT ENTRY TITLE	ORGANISM DATE	ACCESSIONS REFERENCE #author #journa #title

linked to the variable and constant regions of immunoglobulin light chain precursors: implications on the organization and controlled expression of immunoglobulin

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this sequence has since been revised in reference A93822 ##molecule_type protein
#fresidues 21-46, Q', 48-53, B',55-57, 'Z',59-86, 'F', 88-131 #flabel
MCK McKean, D.; Potter, M.; Hood, L. Biochemistry (1973) 12:760-771 Mouse immunoglobulin chains. Pattern of sequence variation among kappa chains with limited sequence differences. 1-35 ##label BUR cross-references MUID: 78235887 ∦cross-references MUID:73140225 ##molecule_type protein B90412 A90374 B90374 ##residues #accession #accession contents ##note contents #authors #journal #title REFERENCE

authors McKean, D.J.; Bell, M.; Potter, M.
journal Proc. Natl. Acad. Sci. U.S.A. (1978) 75:3913-3917
title Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.
cross-references MUID:79012520 REFERENCE #authors #journal

M63; AB22 B93822 contents

1-53;69-107 ##label MC2 ##molecule_type protein ##residues #accession

C93822 #accession

##molecule_type protein #fresidues 21-119,'Y',121-131 ##label MC3 A93204

#authors Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal Nature (1978) 276:785-790
#title Rearrangement of genetic information may produce
immunoglobulin diversity.
#cross-references WUID:79073152 REFERENCE #authors #journal

PC9245; PC4050 C93204 #accession contents

##molecule_type protein
##residues 21-119,'Y',121-131 ##label WEI D93204 #accession

##molecule_type protein
##residues 21-119,'L',121-123,'A',125-129,'L',131 ##label WE2
COMMENT The M63 precursor sequence is shown.
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology FEATURE

#domain signal sequence #status experimental #label SIG #length 131 #molecular-weight 14291 #checksum 5945 Query Match 86.9%; Score 819; DB 2; Length 131; Best Local Similarity 84.7%; Pred. No. 9.95e-77; Matches 111; Conservative 9; Mismatches 11; Indels 0; Gaps 1-20 SUMMARY

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	Mat	Matches	10
DD	Ob		1 metd
KY 121 IFGGEINLEIN 151	Qy		1 MESD
RESULT 4 KVMS32 #type complete ENTRY ITLE IG kappa chain precursor V regions (MOPC 321, TEPC 124) -	d Q	61	22kp ::
mouse Rformal name Mus musculus #common name house mouse 31-May-1979 #sequence_revision 31-May-1979 #text_change	qa	121	tfgs :
ACCESSIONS A90412; A90373; A90374; A01933	Qy	121	TFGG
rs al	RESULT	를 X	r.
<pre>#title Primary structures of N-terminal extra peptide segments linked to the variable and constant regions of immunoglobulin light chain precursors: implications on the</pre>	TITLE ORGANI DATE	TITLE ORGANISM DATE	
uli	ACCE	ACCESSIONS	53
erence	REFE	REFERENCE #authors	irs
#accession A90412 ##molecule_type_protein ##residues 1-37 ##label_BUR ##residues + this premireor was sunthesized in a call_free mustom	•	#journal	lal
75004	•	נונונ	
McKean, D.; Potter, M.; Hood, L. al Biochemistry (1973) 12:749-759	•	acces	#accession ##molecu
<pre>#LILIE</pre>	CLAS	FFI CLASSIFIC KEYWORDS	**resigu CLASSIFICATION KFYWORDS
#contents MOPC 321	FEATURE	TURE	
ule	2	21-131	
##note the partial sequence of the C region of this Bence Jones thote the professional sequence of the C region of this Bence Jones	SUMMARY	IARY	
reported for mouse MOPC 21 only in the transposition of two nearby residues	S &	Query Match Best Local	latch cal S
REFERENCE A90374 #authors McKean, D.; Potter, M.; Hood, L.	Ma	Matches	
#journal Biochemistry (1973) 12:760-771 #title Mouse immunoglobulin chains. Pattern of secuence variation	QQ Q	_	1 metd
among kappa chains with limited sequence differences.	Qy	_	1 MESD
#contents TEPC 124 #accession A90374	qq	61	qqkp
ule ne	Qy	61	OKP.
##note the sequence is compatible with that of MOPC 321 except in having 47-Glx, 51-Trp, and 118-Ala	đ	121	tfgg
The MOPC 321 sequence is shown. Residues 1-20 are the signal se ICATION #superfamily immunoglobul	δy	121	
FEATURE 36-114 #domain immunoglobulin homology #label IMM SUMMARY #length 132 #molecular-weight 14523 #checksum 370	RESULT ENTRY TITLE	트논의	•
Query Match 85.6%; Score 806; DB 2; Length 132; Best Local Similarity 77.1%; Pred. No. 3.08e-75;	ORGAI DATE	ORGANISM DATE	

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Ig kappa chain precursor V region (M-T310) - human (fragment) #formal name Homo sapiens #common name man 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change #superfamily immunoglobulin V region; immunoglobulin homology ö ö Reissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; Lenz, H.; Weiss, E.H.; Rieber, E.P.; Riethmueller, G.; Weidle, U.H. Gene (1992) 121:271-278 Combinatorial functions of two chimeric antibodies directed to human CD4 and one directed to the alpha-chain of the #domain signal sequence #status predicted #label SIGN
#product Iq light chain V region #status predicted
#label MAT gzppklliyrasnlzsgiparfsgsgsrtbftltibpvzabdvatyfczzsbzbpw 120 Gaps 0; Caps JL0073 #type complete
aberrant kappa transcript - mouse
#formal name Mus musculus #common_name house mouse
21.Nov-1993 #sequence_revision 21-Nov-1993 #text_change ; 0 9; Mismatches 10; Indels 85.5%; Score 805; DB 5; Length 131; imilarity 85.5%; Pred. No. 4.01e-75; 20; Mismatches 10; Indels human interleukin-2 receptor. #length 131 #checksum 4648 #type fragment 1-131 ##label WEI immunoglobulin Conservative 2; Conservative 21-Nov-1993 30-Apr-1995 le_type mRNA GTKLEIK 131 HIIIIII SGTKLEIK 131 gtkleik 131 gtkleik 131

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Specific amplification by the polymerase chain reaction of rearranged genomic variable regions of immunoglobulin genes 7 0 1 MESDILLIMVLLLMV-PGSTGDIVLTQSPASLGVSLGQRATISCRASKSVSTSGYSYMHW 59 1 metdtlllwvlllfiipgstgdivltgspaslavslggratisyrasksvstsgysymhw 60 1 metdtlllwvlllwvpgstgdivltgspaslavslggratisyrasksvstsgysymhwn 60 Gaps 61 nqqkpgqpprlliylvsnlesgvparfsgsgsgtdftlnihpveeedaatyycqhire 118 60 YQQKPGQTPKLLIYLASNLESGVPARFSGSGSGTDFTLNIHPUFEEDAATYYCQHSRE 117 S52448 #type complete
Ig kappa chain V region - mouse
#formal name Mus musculus #common name house mouse
08-May-1995 #sequence_revision 21-Jul-1995 #text_change 1; Gaps 61 QQKPCQTPKLLIYLASNLESCVPARFSCSGSCTDFTLNIHPVEEEDAATYYCQHSRE 117 61 qqkpqqpprlliylvsnlesgvparfsgsgsgtdftlnihpveeedaatyycqhire 117 Carroll, W.L.; Mendel, E.; Levy, S. Mol. Immunol. (1988) 25:991-995 Hybridoma fusion cell lines contain an aberrant kappa #length 128 #molecular-weight 14060 #checksum 5564 #length 128 #molecular-weight 14020 #checksum 5468 .; Berdoz, J.; Kraehenbuhl, J.P. submitted to the EMBL Data Library, November 1994 Score 754; DB 11; Length 128; Pred. No. 2.76e-69; Length 128; 6; Indels 5; Indels Score 785; DB 13; Pred. No. 7.84e-73; 4; Mismatches Mismatches from mouse hybridoma cells. S52448 1-128 ##label CAR 1-128 ##label BER #cross-references EMBL:X82689 cross-references MUID:89112230 preliminary preliminary 80.0%; 83.3%; Best Local Similarity 93.2%; Matches 109; Conservative 107; Conservative 21-Jul-1995 transcrip ##molecule_type DNA Best Local Similarity S52445 JL0073 #residues ##residues description submission ##status ##status accession Query Match accession Query Match authors #introns œ ACCESSIONS REFERENCE fauthors journal ACCESSIONS Matches title REFERENCE ORGANISM ORGANISM GENETICS SUMMARY SUMMARY RESULT TITLE ENTRY ENTRY 셤 음 ð 염 ð 셤 ð ð

01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change US-08-137-117B-25.m 11-Aug-1995 A01938 Jul 8 08:18 ACCESS IONS

Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, Nature (1978) 276:785-790 authors

🕯 journal

REFERENCE

title

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Rearrangement of genetic information may produce

immunoqlobulin diversity. cross-references MUID: 79073152

[-111 ##label WEI ##molecule_type protein A01938 #residues #accession

#superfamily immunoglobulin V region; immunoglobulin homology #length 111 #molecular-weight 12039 #checksum 2467 #domain immunoglobulin homology #label IMM\ #disulfide_bonds #status predicted CLASSIFICATION 23-92 SUMMARY FEATURE

Gaps ö DB 2; Length 111; 3; Indels Score 741; DB 2; Pred. No. 8.41e-68; 1; Mismatches Best Local Similarity 96.4%; 78.78; Matches 107; Conservative Query, Match

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divltqspaslavslgqratiscrasksvstsgysymhwyqqkpgqppklliylasnles 60 21 DIVLTQSPASLGVSLGQRATISCRASKSVSTSGYSYMHWYQQKPGQTPKLLIYLASNLES 80 염 ð

111 61 gvparfsgsgsgtdftlnihpveeedaatyycqhsrelprtfgggtkleik 용 ð

#formal name Mus musculus #common name house mouse 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change KVMS75 ORGANISM RESULT

B01938; A01938 30-Sep-1993 A93204 **ACCESSIONS** REFERENCE

Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, Nature (1978) 276:785-790 Rearrangement of genetic information may produce |authors journal #title

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immunoglobulin diversity #cross-references MUID:79073152 B01938 #accession

1-111 ##label WEI #superfamily immunoglobulin homology immunoglobulin ##molecule_type protein ##residues CLASSIFICATION KEYWORDS

FEATURE

#length 111 #molecular-weight 12010 #checksum 2086 Score 734; DB 2; Length 111; Pred. No. 5.30e-67; #disulfide_bonds #status predicted 77.98; Query Match 23-92 SUMMARY

9 1 divltqspaslavslgqratiscrasksvstsgysymhwyqqkpgqppklliylasnles 21 DIVLIQSPASLGVSLGQRATISCRASKSVSTSGYSYMHWYQQRDGQTPKLLIYLASNLES g

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Gaps

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Mismatches

Best Local Similarity 94.6%;

105; Conservative

Matches

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GVPARFSGSGSGTDFTLMIHPVEEEDAATYYCQHSRENPYTFGGGTKLEIK 131 81

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f-111 ##label WEI # featon; immunoglobulin homology #superfamily immunoglobulin V region; immunoglobulin homology
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                                                                                                                                                            Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, Nature (1978) 276:785-790
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                                                           #formal_name Mus musculus #common_name house mouse
30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
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Pred. No. 2.09e-65;
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Pred. No. 5.63e-66;
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                   disulfide bonds *status predicted
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Application of (13)C NMR spectroscopy to paratope mapping for Kim, H.H.; Kato, K.; Yamato, S.; Igarashi, T.; Matsunaga, C.; ö Sequence and linkage of the V(kappa)21A and G germ-line gene Ohtsuka, H.; Higuchi, A.; Nomura, N.; Noguchi, H.; Arata, 9 21 DIVLIÇEPASLGVSLGQRATISCRASKSVSTSGYSYMHWYQQKPQQTPKLLIYLASNLES 80 Gaps #formal name Mus musculus #common name house mouse 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995 806731 545715 #type complete
antigen-Fab VL - Pseudomonas aeruginosa
#formal_name Pseudomonas aeruginosa
10-Dec-1994 #sequence_revision 10-Dec-1994 #text_change 21 DIVLIQSPASLGVSLGQRATISCRASKSVSTSGYSYMHWYQQKPGQTPKLLIYLASNLES 1 divltqspaslavslgqratiscrasksvstsgysymhwyqqkpgqpprlliylasnles preliminary 1-112 ##label KIM #length 112 #molecular-weight 12168 #checksum 6129 ö 61 gvparfsgssgstdftlniqpveeedaaiyycqhsrelpltfgagtklelk 111 Length 112; 5; Indels Alanen, A.; Weiss, S. Eur. J. Immunol. (1989) 19:1961-1963 Query Match 75.7%; Score 713; DB 12; Best Local Similarity 91.0%; Pred. No. 1.31e-64; 5; Mismatches Ig kappa chain precursor - mouse larger antigen-Fab complexes. FEBS Lett. (1994) 346:246-250 #type complete segments in the mouse 1-120 ##label ALA ##cross-references EMBL:X16955 fcross-references MUID:90060210 preliminary Matches 101; Conservative 10-Dec-1994 ##molecule type DNA 506731 S45714 506731 S45715 ##residues ##residues #introns CLASSIFICATION SUMMARY ##status ##status #accession *accession 13 12 fauthors | journal authors f journal **ACCESSIONS** ACCESSIONS #title ftitle REFERENCE TITLE ORGANISM REFERENCE ORGANISM GENETICS SUMMARY RESULT TITLE ENTRY 염 셤 ð 셤 à ð ð

#superfamily immunoglobulin V region; immunoglobulin homology #length 120 #molecular-weight 13029 #checksum 5418

DB 5; Length 120;

75.1%; Score 707;

Query Match

1 divltqspaslavslgqratiscrasksvstsgysymhwyqqkpgqppklliylassles 60

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#superfamily immunoglobulin V region; immunoglobulin homology 2; :: anti-mouse red blood submitted to the EMBL Data Library, September 1991 Cloning and sequencing of the CDNA coding for the variable regions of the heavy and light chains of two monoclonal 61 yqqkpgqppklliyaasnvesgvparfsgsgsgtdfslnihpveeddiamyfcqqsrkvp 120 60 YQQKPGQTPKILIYIASNLESGVPARFSGSGSGTDFTINIHPVEEEDAATYYCQHSRENP 119 Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, 1 divltqspaslavslgxratlscrasqsvsssgysymhwyqqkpqqspklliky-asnle 59 21 DIVLTQSPASLGVSLGQRATISCRASKSVSTSGYSYMHWYQQKPGQTPKLLI-YLASNLE 79 1 mesdtlllwvlllwvpggstgdivltgspaslavslggratiscrasesveyygtslmgw 60 Gaps #formal name Mus musculus #common name house mouse 30-Sep-1993 #sequence_revision 12-Feb-1993 #text_change 30-Sep-1993 Gaps 509963 #type fragment Ig kappa chain V-J region (103-7E) - mouse (fragment) 1; 5; 60 sgvparfsgsgsgtdftlnihpveeedtatyycqhsweipytfgggtkleik 111 80 SGVPARFSGSGSGTDFTINIHPVEEEDAATYYCOHSRENPYTFGGGTKLEIK 131 #journal Eur. J. Immunol. (1990) 20:771-777
#title Variable region sequences of pathogenic anti-mo#cross-references MUID:90269328
#accession S09963 Score 703; DB 5; Length 111; Pred. No. 1.81e-63; Indels 3; Indels antibodies to the estrogen receptor. Pred. No. 6.33e-64; 7; Mismatches 12; Mismatches #length 111 #checksum 3824 1-111 ##label REI 1-110 ##label MON ##cross-references EMBL:X62703 ##cross-references EMBL:X51851 ##molecule_type mRNA ##residnon Moncharmont, B. Query Match 74.6%; Best Local Similarity 90.2%; Best Local Similarity 83.3%; 12-Apr-1995 S24288 101; Conservative 100; Conservative ##molecule_type mRNA 809963 \$24288 S24287 S09955 S09963 ##residues description CLASSIFICATION submission faccession | 14 12 authors #authors ACCESSIONS ACCESSIONS Matches Matches REFERENCE REFERENCE ORGANISM ORGANISM SUMMARY RESULT TITLE ENTRY DATE g 셤 g 유 ð ð ð δ

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immunoglobulin V region; immunoglobulin homology #molecular-weight 12055 #checksum 9833 #superfamily i CLASSIFICATION SUMMARY

Gaps 6; Indels 1; 74.4%; Score 701; DB 5; Length 110; 91.9%; Pred. No. 3.05e-63; 2; Mismatches Best Local Similarity 91.9%; 102; Conservative Query Match Matches

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1 digitqspaslavslgqratisyrasksvstsgysymhwnqqkpgqpprlliylvsnles 60 용 ò

61 gvparfsgsgsgtdftlnihpveeedaatyycqhire-pytfgggtkleik 110

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81 GVPARFSGSGSGTDFTLNIHPVEEEDAATYYCQHSRENPYTFGGGTKLEIK 131

Search completed: Mon Jul 8 08:28:44 1996 Job time : 21 secs.

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPerch pp

Mon Jul 8 08:27:52 1996; MasPar time 4.29 Seconds 468.611 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-137-117B-25 (1-131) from US08137117B.pep 942 1 MESDTLLIMVLLIMVPGSTG........CQHSRENPYTFGGGTKLEIK 131 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

43470 seqs, 15335248 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot31
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8

Mean 41.444; Variance 73.478; scale 0.564 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	1.27e-158	1.36e-155	1.74e-140	7.28e-139	8.86e-137	1.27e-135	2.67e-127	3.18e-125	1.56e-124	1,31e-123	6.42e-123	5.35e-122	9.10e-122
		CHAIN PRECUR	HAIN PRECUR	CHAIN V-III	CHAIN V-III	HAIN V-III	HAIN V-III	HAIN V-III	HAIN V-III	HAIN V-III	HAIN V-III	HAIN V-III	CHAIN V-III	CHAIN V-III
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	89	4	4	4	4	4	4	4	4	4	4	4	4	4
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₀ ∤∘	Query Match	86.9	85.6	78.7	77.9	77.0	76.4	72.6	71.7	71.3	70.9	70.6	70.2	70.1
	Score	819	908	741	734	725	720	684	675	672	899	999	661	099
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14	929	9.69	111	7	KV3Q MOUSE	IG KAPPA	CHAIN	V-111	7.58e-121
15	649	68.8	110	Þ	KV3P_MOUSE	IG KAPPA	CHAIN	V-III	-11
16	646	9.89	111	4	KV3K MOUSE	IG KAPPA	CHAIN	V-III	1.52e-118
17	640	6.79	111	4	KV3C_MOUSE	IG KAPPA	CHAIN	V-111	3.63e-117
18	634	67.3	111	4	KV3D_MOUSE	IG KAPPA	CHAIN	V-III	8.68e-116
19	634	67.3	112	Þ	KV3B_MOUSE		CHAIN	V-III	8.68e-116
20	632	67.1	111	4	KV3A_MOUSE	IG KAPPA		V-111	2.50e-115
21	622	96.0	112	Þ	KV3G MOUSE	IG KAPPA	CHAIN	V-111	4.93e-113
22	593	63.0	111	4	KV3E_MOUSE	IG KAPPA	CHAIN	V-III	2.16e-106
23	280	61.6	129	4	KV3M_HUMAN	IG KAPPA	CHAIN	PRECUR	2.01e-103
24	578	61.4	129	4	KV3L HUMAN	IG KAPPA	CHAIN	PRECUR	5.75e-103
25	573	8.09	133	4	KV2F HUMAN	IG KAPPA	CHAIN	PRECUR	7.96e-102
26	571	9.09	133	4	KV4B HUMAN	IG KAPPA	CHAIN	PRECUR	27e-
27	268	60.3	134	4	KV4C HUMAN	IG KAPPA	CHAIN	PRECUR	10e-
78	549	58.3	129	4	KV3H_HUMAN		CHAIN	PRECUR	2.32e-96
53	539	57.2	128	4	KV3K_HUMAN	IG KAPPA	CHAIN	PRECUR	33e-9
30	534	56.7	129	4	KV1W HUMAN				5.91e - 93
31	529	56.2	114	4	KV4A HUMAN		CHAIN		8.03e - 92
32	226	55.8	115	4	KV3I HUMAN	IG KAPPA	CHAIN		84e-
33	521	55.3	117	4	KV2E HUMAN	IG KAPPA	CHAIN	PRECUR	5.21e-90
34	517	54.9	121	4	KV40 HUMAN		_	PRECU	19e-
35	516	54.8	113	4	KV2B_HUMAN				05e-
36	510	54.1	108	4	KV5P_MOUSE	_		V-V	-909
37	509	54.0	112	4	KV2D_MOUSE				70e-
38	209	マ	116	4	KV3J HUMAN			PRECU	70e-
39	208	ന	113	4	KV2E_MOUSE		CHAIN	V-II	
40	504	53.5	113	4	KV2F MOUSE		CHAIN	V-II R	, 63e-
41	200	m	112	4	KV2C HUMAN	IG KAPPA	CHAIN	V-11	-906
42	499	ന	113	4	KV2D HUMAN	IG KAPPA	CHAIN		4.88e-85
43	499	53.0	113	4	KV2G MOUSE		CHAIN	V-11	4.88e-85
44	491	\sim	129	4	KV1X_HUMAN	IG KAPPA	CHAIN	PRECUR	10e-
45	489	51.9	136	4	KV5B_MOUSE	IG KAPPA	CHAIN	PRECUR	8.75e-83

ALI GNMENTS

								MAMMALIA;																			
	KV3I MOUSE STANDARD; PRT; 131 AA.	P01661;	21-JUL-1986 (REL. 01, CREATED)	1-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)	1-0CT-1993 (REL. 27, LAST ANNOTATION UPDATE)	IG KAPPA CHAIN PRECURSOR V-III REGION (MOPC 63).	MUS MUSCULUS (MOUSE).	UKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	RODENTIA; RODENTIA.	SEQUENCE OF 1-35.	78235887	BURSTEIN Y., SCHECHTER I.;	BIOCHEMISTRY 17:2392-2400(1978).	2]	SEQUENCE OF 21-131.	73140225	CKEAN D.J., POTTER M., HOOD L.E.;	BIOCHEMISTRY 12:760-771 (1973).	[3]	REVISIONS.	79012520	MCKEAN D.J., BELL M., POTTER M.;	PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).	PIR; A01935; KVMSM6.	HSSP; P01679; 1ACY.	IMMUNOGLOBULIN V REGION; SIGNAL.	
RESULT 1	11			DT 2		田		20	30	RP .0	W.			RN	짪	æ	RA	RL I		쭚	RW.	RA		H	DR F	Σ	

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SIGNAL	**	FT DOMAIN FT DISULFID		Query Match	Best Local Si Matches 101	Db 1 metdt	Qy 1 MESDT	Db 61 zzkpg	Qy 61 QQKPG	Db 121 tfgsg	Qy 121 TFGGG	RECIII	V3R			 OC EUKARYOTA; OC EUTHERIA;		 DR PIR; A0193 DR HSSP: P016	KW IMMUNOGLOB	FT DOMAIN	 FI DOMAIN	FT DISULFID FT NON TER	SQ SEQUENCE	Query Match Best Local Si	-0	•	Qy 21 DIVLT	Db 61 gvpar	01 C/03/0
		SIGNAL 1 20 CHAIN 21 131 IG	DOMAIN 44 58	DOMAIN 59 73 FRAMEWORK 2. DOMAIN 74 80 COMPLEMENTARITY-DETERMINING	DOMAIN 81 112 FRAMEWORK 3. DOMAIN 113 121 COMPLEMENTARITY-DETERMINING	DOMAIN 122 131 DISULFID 43 112	NON TER 131 131 SEQUENCE 131 AA; 14291 MW;	86.9%; Score 819; DB 4;	o4./*; Fred. No. 1.2/9-130; rvative 9; Mismatches 11; Indels 0; Gaps	1 metdtlllwvlllwvpgstgnivltqspaslavslggratiscrasesvdsygnsfmhwy	1 MESDTILIMVILIMVPGSTGDIVLTQSPASLGGVSLGQRATISCRASKSVSTSGYSYMHMY	61	61	121	121	2 V3F MOUSE STANDARD: PRT:				 			_			SIGNAL 1 20	CHAIN 21 132 DOMAIN 21 43	DOMAIN 44 58 DOMAIN 59 73	DA NT MANAGE

Db 61 gvparfsgsgsgtdftlnihpveeedaatyycqhsrelprtfgggtkleik 111	Qy 21 DIVLTQSPASLGVSLGQRATISCRASKSVSTSGYSYMHWYQQKPGQTPKLLIYLASNLES 80	DOMAIN 1 23	
21 DIVLTQSPASLGVSLGQRATISCRASKSVSTSGYSYMHWYQQKPGQTPKLLIYLASNLES		DOMAIN 24 38 DOMAIN 39 53 DOMAIN 39 53 DOMAIN 66 DOMAIN 61 92 DOMAIN 102 111 DOMAIN 102 111 SEQUENCE 111 A2; 1239 MW; Sury Match 78.7%; S Best Local Similarity 96.4%; P Matches 107; Conservative	DOMAIN 1 23 FRAMEWORK 1.
1 divltgspaslavslggratiscrasksvstsgysymhwygqkpgppklljylasnles 	1 divltgspaslavslggratiscrasksvetsgysymhwygdkpggppklljylasnles	DOMAIN 24 38 COMPLEMENTARITY-DETERMINING DOMAIN 39 53 FRAMEWORK 2. DOMAIN 61 92 FRAMEWORK 3. DOMAIN 93 101 COMPLEMENTRITY-DETERMINING DOMAIN 102 111 FRAMEWORK 4. DISULFID 23 92 BY SIMILARITY. NON TER 111 111 111 SEQUENCE 111 Aa; 12039 Mm; 66692 CN;	DOMAIN 1 23 FRAMEWORK 1. DOMAIN 24 38 COMPLEMENTARITY-DETERMINING DOMAIN 39 53 FRAMEWORK 2. DOMAIN 54 60 COMPLEMENTARITY-DETERMINING DOMAIN 61 92 FRAMEWORK 3. DOMAIN 102 111 FRAMEWORK 4. DISULFID 23 92 BY SIMILARITY. NON TER 111 111 111 SEQUENCE 111 AA; 12039 MM; 66692 CN;
Query Match 78.7%; Score 741; DB 4; Length 111; Best Local Similarity 96.4%; Pred. No. 1.74e-140; Matches 107; Conservative 1; Mismatches 3; Indels 0; Gaps 1 divltgspaslavslggratiscrasksvstsgysymhwyqqkpqqppklliylasnles 60	Duery Match 78.7%; Score 741; DB 4; Length 111; Bost Local Similarity 96.4%; Pred. No. 1.74e-140; Matches 107; Conservative 1; Mismatches 3; Indels 0; Gaps 1 divltgspaslavslggratiscrasksvstsgysymhwygdkpggppklliylasnles 60	DOMAIN 24 38 COMPLEMENTARITY-DETERMINING DOMAIN 39 53 FRAMEWORK 2. DOMAIN 64 60 COMPLEMENTRITY-DETERMINING DOMAIN 61 92 FRAMEWORK 3. DOMAIN 93 101 COMPLEMENTARITY-DETERMINING DOMAIN 102 111 FRAMEWORK 4. DISULFID 23 92 BY SIMILARITY.	DOMAIN
NON TER 111 111 SEQUENCE 111 AA; 12039 MW; 66692 CN; Query Match 78.7%; Score 741; DB 4; Length 111; Best Local Similarity 96.4%; Pred. No. 1.74e-140; Matches 107; Conservative 1; Mismatches 3; Indels 0; Gaps 1 divltqspaslavslqqratiscrasksvstsgysymhwyqqkpqqpklliylasnles 60 1 divltqspaslavslqqratiscrasksvstsgysymhwyqqkpqqppklliylasnles 60 21 DIVLTQSPASLGVSLGQRATISCRASKSVSTSGYSYMHWYQQKPQTPKLLIYLASNLES 80	NON TER 111 111 SEQUENCE 111 AA; 12039 MW; 66692 CN; Query Match 78.7%; Score 741; DB 4; Length 111; Best Local Similarity 96.4%; Pred. No. 1.74e-140; Matches 107; Conservative 1; Mismatches 3; Indels 0; Gaps 1 divltqspaslavslgqratiscrasksvstsgysymhwyqqkpqqppklliylasnles 60	DOMAIN 24 38 COMPLEMENTARITY-DETERMINING DOMAIN 39 53 FRAMEWORK 2. DOMAIN 54 60 COMPLEMENTARITY-DETERMINING DOMAIN 61 92 FRAMEWORK 3. DOMAIN 93 101 COMPLEMENTARITY-DETERMINING	DOMAIN 1 23 FRAMEWORK 1. DOMAIN 24 38 COMPLEMENTARITY-DETERMINING DOMAIN 39 53 FRAMEWORK 2. DOMAIN 54 60 COMPLEMENTARITY-DETERMINING DOMAIN 61 92 FRAMEWORK 3. DOMAIN 93 101 COMPLEMENTARITY-DETERMINING
DOMAIN 102 111 FRAMEWORK 4.	DOMAIN 102 111 FRAMEWORK 4.	DOMAIN 24 38 COMPLEMENTARITY-DETERMINING DOMAIN 39 53 FRAMERORK 2. DOMAIN 54 60 COMPLEMENTARITY-DETERMINING DOMAIN 61 92 FRAMERORK 3.	DOMAIN
DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.	DOWAIN DOMAIN 102 111 FRAMEWORK 4. DISULEID 23 92 BY SIMILARITY. NON TER 111 111 SEQUENCE 111 Aa; 12039 MW; 66692 CN; Query Match 78.7%; Score 741; DB 4; Length 111; Best Local Similarity 96.4%; Pred. No. 1.74e-140; Matches 107; Conservative 1; Mismatches 3; Indels 0; Gaps 1 divltqspaslavslgqratiscrasksvstsgysymhwyqqkpqqppklliylasnles 60	DOMAIN 24 38 COMPLEMENTARITY-DETERMINING DOMAIN 39 53 FRAMEWORK 2.	DOMAIN
DOMAIN	DOMAIN 34	DOMAIN 24 38 COMPLEMENTARITY-DETERMINING	DOMAIN 24 38 COMPLEMENTARITY-DETERMINING
DOMAIN 39 53 FRAMEWORK 2.	DOMAIN 39 53 FRAMEWORK 2.		DOMAIN 1 23
HSSP; PO16/9; IACY.	HSSP; PO16/9; PACY. IMMUNOGLOBULIN V REGION. DOMAIN	_	
PR8 PRAMENOR PRAMENOR PRAMENOR PR8 PRAMENOR PR8 PRAMENOR PR8 PRAMENOR PR8	PIR, ROUBS84, HSD85; KVMS84, HSD95; LACY. LAMUNOCLOBULN V RECION. PRAMEWORK 1. DOMAIN		
MEIGRIT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.; NATURE 716:792-790(1978). PIR, A01938; KWAS84. HSSP; PO1679; 1ACY. IMMUNOGLOBULIN V REGION. DOMAIN 1 23 FRAMEWORK 1. DOMAIN 24 53 COMPLEMENTARITY-DETERMINING 1. DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2. DOMAIN 61 92 FRAMEWORK 3. DOMAIN 61 92 FRAMEWORK 4. DOMAIN 102 111 FRAMEWORK 4. DISULFID 23 92 BY SIMILARITY. DOMAIN 102 111 FRAMEWORK 4. DISULFID 23 92 BY SIMILARITY. ANN TER 111 111 SEQÜENCE 111 AA; 12039 MM; 66692 CN; Set Local Similarity 96.4%; Pred. No. 1.74e-140; 4atches 107; Conservative 1; Mismatches 3; Indels 0; Gaps 1 divltqspaslavs1gqratisCrasksvstsgysymhwyqqkpqqppklliylasnles 60 HillillIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	WEIGERT M., GATMATTAN L., LOH E., SCHILLING J., HOOD L.E.; NATURE 276:785-790(1978). PISP, A01938 KYMS84. HSSP; PO1679; LACY. LAWINOGLOBULIN V REGION. DOMAIN	WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E. NATURE 276:785-790(1978). PIR, Å01938; KVMS84. HSSP, P01679; IACY. IMMINGACIORITIN V PRETON	WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E. NATURE 276:785-790(1978). PIR, A01938; KVMS84.
SEQUENCE.	SEQUENCE. 79073152 WEIGERT M., GATWAITAN L., LOH E., SCHILLING J., HOOD L.E.; NATURE 276:785-790(1978). PRI, A01398; KVMS84. HSSP; P01679; 1ACY. IMMUNOGLOBULIN V REGION. DOMAIN 1 23 COMPLEMENTARITY-DETERMINING 1. DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1. DOMAIN 39 53 FRAMEWORK 1. DOMAIN 61 92 FRAMEWORK 3. DOMAIN 61 92 FRAMEWORK 4. DOMAIN 102 111 FRAMEWORK 4. DISULED 23 101 COMPLEMENTARITY-DETERMINING 3. DOMAIN 102 111 FRAMEWORK 4. DISULED 23 9 BY SIMILARITY. NON TER 111 111 SEQÜENCE 111 AA; 12039 MM; 66692 CN; Best Local Similarity 96.4%; Pred. No. 1.74e-140; Matches 107; Conservative 1; Mismatches 3; Indels 0; Gaps 1 divitgapaslavslggratiscrasksvstegypymhwyqqkpqppkiliylasnles 60	SEQUENCE. SEQUENCE. WEIGENT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E. NATURE 276:785-790(1978). PIR, A01938; KYMS84. THASP; PO1679; LACY. THANTAGCORITIN V PECTON	SEQUENCE. 1973152 WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E. NATURE 276:785-790(1978). PIR, À01938; KVMS84.
11 SEQUENCE. 35 36 37 37 38 38 39 39 39 39 39 39	11 SEQUENCE. 99018152 WEIGERT M., GATWAITAN L., IOH E., SCHILLING J., HOOD L.E.; NATURE 276:785-790(1978). PIR, A01938, KVMS84. HSSP, P01679, 1ACY. IMMUNOGLOBULIN V REGION. DOMAIN	(1) SEQUENCE. 19073152 WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E. NATURE 276:785-790(1978). PIR, A01938; KYMS84. THMSPR, PO1679; LACY. THMSPROCORDITIN V BEGIN	(1) SEQUENCE. 1907315. WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E. NATURE 276:785-790(1978). PIR, À01938; KVMS84.
EUTHERIA; RODENTIA. [1] SEQUENCE. 19071817 SEQUENCE. 19071815.2 WILLING J., HOOD L.E.; NATURE 2/6:785-790(1978). PIR, A01938; KVMS84. HSSP; PO1679; LACY. IMMUNGLOBULIN V REGION. DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1. DOMAIN 39 53 FRAMEWORK 1. DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2. DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 3. DOMAIN 61 92 FRAMEWORK 3. DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3. DOMAIN 102 111 FRAMEWORK 4. DOMAIN 102 111 MA; SCORE 741; DB 4; Length 111; SEQUENCE 111 AA; 12039 MW; 66692 CN; Matche 107; Conservative 1; Mismatches 3; Indels 0; Gaps 1 divltgspaslavslggratiscrasksvstsgysymhwyqqkpgqppklliylasnles 60 111fifill[EUTHERIA; MEDENTIA. [1] EUTHERIA; MEDENTIA. [1] SEQUENCE. 1907315. WEIGERT M., GATWALTAN L., LOH E., SCHILLING J., HOOD L.E.; NATURE 276:785-790(1978). PTR; A01938; KYMS84. HSSP; POL679; LACY. IMMUNOCLOBLIN V REGION. DOMAIN 1 24 38 COMPLEMENTARITY-DETERMINING 1. DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1. DOMAIN 39 53 FRAMEWORK 1. DOMAIN 61 92 FRAMEWORK 3. DOMAIN 61 92 FRAMEWORK 3. DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 2. DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3. DOMAIN 102 111 FRAMEWORK 4. DISULEID 23 92 BY SIMILARITY. NON TER 111 111 SEQÜENCE 111 AA; 12039 MM; 66692 CN; SEQÜENCE 111 AA; 12039 MM; 66692 CN; MATCH	EUTHERIA; METAZOA; CHOKUAIA; VEKIEBKATA; EUTHERIA; RODENTIA. [1] SEQUENCE. 1907315.2 WEIGERT M., GATWAITAN L., LOH E., SCHILLIN NATURE 276:785-790 (1978). PIR; Å01938; KVMS84.	EGNARIOTA, METAZOA, CHORDATA, VERTEBRATA, EUTHERIA, RODENTIA. [1] SEQUENCE. 79073152 WEIGERT M., GATMAITAN L., LOH E., SCHILLIN NATURE 276:785-790 (1978). PIR, A01938; KVMS84.
MUS MOUSEL). EUTHERIA; RODENTIA. [1] EUTHERIA; RODENTIA. [1] SEQUENCE. 19073152 WEICERT M. GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.; NATURE 276:785-790 (1978). PTR; A01938; KYMS84. HSSP; POL679; LACY. IMMUNCGLOBULIN V REGION. DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1. DOMAIN 39 53 FRAMEWORK 1. DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2. DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3. DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3. DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3. DOMAIN 93 101 COMPLEMENTARITY. DOMAIN 93 101 MAICH 111; REAMEWORK 4. DISULTO 3. DOMAIN 111 111 SEQUENCE 111 AA; 12039 MW; 66692 CN; Reatches 107; Conservative 1; Mismatches 3; Indels 0; Gaps 1 divitqspaslavslqqratiscrasksvstsgysymhwyqqkpqqppklliylasnles 60 I divitqspaslavslqqratiscrasksvstsgysymhwyqqkpqqppklliylli I divitqspaslavslqqratiscrasksvstsgysymhwyqqkpqqppklliylli 21 DIVLTqSpaslavslqqratiscrasksvstsgysymhwyqqkpqqppklliylli 21 DIVLTqSpaslavslqqratiscrasksvstsgysymhwyqqkpqqppklliylli 21 DIVLTqSPASLGVSTSGYSYSYSYSYSYSYSYSYSYSYSYSYSYSYSYSYSYS	MUS MUSCULUS (MOUSE). EUTHERIA; MUSCULUS (MOUSE). (1) EUTHERIA; RODENTIA. (1) SEQUENCE. 79073152 WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.; NATURE 276:785-790(1978). PIR; A01388; KYMS84. HSSP; P01679; 1ACY. IMMUNOGLOBULIN V REGION. DOMAIN 1 23 COMPLEMENTARITY-DETERMINING 1. DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1. DOMAIN 39 53 FRAMEWORK 1. DOMAIN 61 92 FRAMEWORK 3. DOMAIN 61 92 FRAMEWORK 4. DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3. DOMAIN 102 111 FRAMEWORK 4. DISULED 23 92 FRAMEWORK 4. DISULED 23 92 BY SIMILARITY. NON TER 111 111 SEQÜENCE 111 AA; 12039 MM; 66692 CN; Rest Local Similarity 96.4%; Pred. No. 1.74e-140; Matches 107; Conservative 1; Mismatches 3; Indels 0; Gaps 1 divltqspaslavslggratiscrasksvstegysymhwyqqkpqppklljylasnles 60	MUS MUSCOLUS (MOUSE). EUTHERIA; METAZOA, CHORDATA; VERTEBRATA; EUTHERIA; RODENTIA. [1] SEQUENCE. 79073152 WEIGERT M., GATWAITAN L., LOH E., SCHILLIN NATURE 276:785-790(1978). PIR; A01938; KVMS84. HSSP, POLGT9; IACY. WARRACCIORITIN V PECTON	MUS MUSCOLUS (MOUSE). EUTHERIA; METAZOA, CHORDATA; VERTEBRATA; EUTHERIA; RODENTIA. [1] SEQUENCE. 79073152 WEIGERT M., GATMAITAN L., LOH E., SCHILLIN NATURE 276:785-790 (1978). PIR; A01938; KVMS84.
01-OCT-1993 (REL. 27, IAST ANNOTATION UPDATE) IG KAPPA CHANN V-III RECION (PC 6684). MUS MUSCULUS (MOUSE). EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAWALIA; EUTHERIA; RODENTIA. [1] SEQUENCE. 19073152 WEICERT M., GATWAITAN L., IOH E., SCHILLING J., HOOD L.E.; NATURE 276:785-790(1978). PIX, A01385; KWS84. HSSP; PO1679; LACY. IMMUNOGLOBULIN V REGION. DOMAIN 1 23 COMPLEMENTARITY-DETERMINING 1. DOMAIN 39 53 COMPLEMENTARITY-DETERMINING 2. DOMAIN 39 53 FRAMENORK 2. DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2. DOMAIN 61 92 FRAMENORK 3. DOMAIN 102 111 FRAMENORK 4. DISULFID 23 92 BY SIMILARITY. DISULFID 24 BY SIMILARITY. DISULFID 25 BY SIMILARI	01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE) IG KAPPA CHAIN V-III REGION (PC 6684). MUS MUSCULUS (MOUSE). EUTHERIA; RETAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; RODENTIA. [1] SEQUENCE. 79073152 WEIGERT M., CATMALTAN L., LOH E., SCHILLING J., HOOD L.E.; NATURE 276:785-790(1978). PIR, A01938; KVMS84. HSSP; PO1679; LACY. IMMUNOGLOBULIN V REGION. DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1. DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 2. DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2. DOMAIN 61 92 FRAMEWORK 2. DOMAIN 61 92 FRAMEWORK 3. DOMAIN 61 92 FRAMEWORK 4. DISULEID 23 99 101 COMPLEMENTARITY-DETERMINING 3. DOMAIN 102 111 FRAMEWORK 4. DISULEID 23 97 FRAMEWORK 4. DISULEID 23 97 FRAMEWORK 3. DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3. DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3. DOMAIN 102 111 FRAMEWORK 4. DISULEID 23 99 FRAMEWORK 4. DISULEID 23 97 FRAMEWORK 3. DISULEID 23 99 FRAMEWORK 4. DISULEID 23 97 FRAMEWORK 4. DISULEID 23 91 BY SIMILARITY. NON TER 111 111 SEQÜENCE 111 AA; 12039 MM; 66692 CN; MATCHER 107; CONSELVATIVE 1; MISMATCHER 3; Indels 0; Gaps 1 divitqspaslavslgratiscrasksvstegysymhwyqdxpdppklliylasnles 60	01-OCT-1993 (REL. 27, LAST ANNOTATION UPDB IG KAPPA CHAIN V-III RECION (PC 6684). MUS MUSCULUS (MOUSE). EUTHERIA; METAZOA; CHONDATA; VERTEBRATA; EUTHERIA; RODENTIA. [1] SEQUENCE. 79073152 WEIGERT M., GATMAITAN L., LOH E., SCHILLIN NATURE 276:785-790(1978). PTR; A01938; KYMS84. HSSP; P01679; IACY. WARTMACHORITIN U PESTON	01-OCT-1993 (REL. 27, LAST ANNOTATION UPDB IG KAPPA CHAIN V-III RECION (PC 6684). MUS MUSCULUS (MOUSE). EUTRARYOTA; METAZOA; CHORDATA; VERTEBRATA; EUTHERIA; RODENTIA. [1] SEQUENCE. 1907315.2 WEIGERT M., GATMAITAN L., LOH E., SCHILLIN NATURE 276:785-790 (1978). PIR; A01938; KVMS84.
21-JUL-1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE) 1G KAPPA (CHAIN V-III RECION (PC 6684). MUS MUSCULUS (MOUSE). EUKARATORI, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; RODENTIA. 1	21-JUL-1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE) 1G KAPPA CHAIN V-111 REGION (PC 6684). MUS MUSCULUS (MOUSE). EUTHERIA; RODENTIA. [1] SEQUENCE. 19073152 WITCERT M., GATMAITAN L., IOH E., SCHILLING J., HOOD L.E.; NATURE 276:785-790(1978). PIR; A01938; KVMS84. HSSP; PO1679; LACY. IMMUNGLOBULIN V REGION. DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1. DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 2. DOMAIN 39 53 FRAMENORK 1. DOMAIN 61 92 FRAMENORK 3. DOMAIN 61 92 FRAMENORK 3. DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3. DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3. DOMAIN 102 111 FRAMENORK 4. DISULEID 23 92 BY SIMILARITY. NON TER 111 111 SEQÜENCE 111 AA; 12039 MM; 66692 CN; MATCH 78.78; SCORE 741; DB 4; Length 111; SEQÜENCE 111 AA; 12039 MM; 66692 CN; MATCH 111 111 III IIII IIII IIII IIII IIII	21-JUL-1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 01, LAST SEQUENCE UDDATE 31-JUL-1986 (REL. 01, LAST SEQUENCE UDDATE 01 COCT-1993 (REL. 27, LAST ANNOTATION UPPA IG KAPPA CHAIN V-III REGION (PC 6684). MUS MUSCULUS (MOUSE). EUTHRIA; RODENTIA. [1] SEQUENCE. 1907315.2 WEIGERT M., GATWAITAN L., LOH E., SCHILLIN NATURE 276:785-790 (1978). PIR; À01338; KVMS84. WEIGERT M., UPFINN NATURE 276:785-790 (1978).	21-JUL-1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 01, LAST SEQUENCE UDDATE O1-OCT-1993 (REL. 27, LAST ANNOTATION UPDA IG KAPPA CHAIN V-III REGION (PC 6684). MUS MUSCULUS (MOUSE). EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; EUTHRIA; RODENTIA. [1] SEQUENCE. 79073152 WEIGERT M., GATMAITAN L., LOH E., SCHILLIN NATURE 276:785-790 (1978). PIR; À01938; KVMS84.
KV3R MOUSE STANDARD; PRT; 111 AA. 21-JUL-1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 11-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 12-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 13-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE) 14-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE) 15-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE) 16-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE) 17-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE) 18-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE) 18-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE) 18-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE) 19073152 19073152 19073152 19073152 19073154 19073157 1909AIN 1 23 FRAMEWORK 1. 1909AIN 39 53 FRAMEWORK 2. 1909AIN 54 60 COMPLEMENTARITY-DETERMINING 2. 1909AIN 53 FRAMEWORK 3. 1909AIN 61 92 FRAMEWORK 4. 1909AIN 61 92 FRAMEWORK 4. 1919 (REL 11) 11 FRAMEWORK 4. 1919 (REL 11) 11 REPAREMORK 1. 1910 (REL 11) 11 REPAREMORE 1	KV3R MOUSE STANDARD; PRT; 111 AA. PULTON; 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE) 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE) 00-OMAIN 1 23 COMPLEMENTARITY-DETERMINING 1. 00-OMAIN 24 38 COMPLEMENTARITY-DETERMINING 2. 00-OMAIN 24 38 COMPLEMENTARITY-DETERMINING 3. 00-OMAIN 54 60 COMPLEMENTARITY-DETERMINING 3. 00-OMAIN 54 60 COMPLEMENTARITY-DETERMINING 3. 00-OMAIN 54 60 COMPLEMENTARITY-DETERMINING 3. 00-OMAIN 61 92 FRAMEWORK 2. 00-OMAIN 61 92 FRAMEWORK 3. 00-OMAIN 102 111 FRAMEWORK 4. 013 102 111 FRAMEWORK 4. 013 11 111 111 SEQUENCE 111 AA; 12039 MM; 66692 CN; 01 SEQUENCE 111 AA; 12039 MM; 66692 CN; 01 AARCHE 111 111 111	KVJR MOUSE STANDARD; PRT; 111 A POLGTO, 1 CL-JUL-1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDA IG KAPPA CHAIN V-III RECION (PC 6684). MUS MUSCULUS (MOUSE). EUTHERIA; RODENTIA. [1] SEQUENCE. 79073152 WEIGERT M., GATMAITAN L., LOH E., SCHILLIN NATURE 276:785-790(1978). PR; A01938; KVMS84. 1 MATURE 276:785-790(1978).	KV3R MOUSE STANDARD; PRT; 111 PRO1670; 21-JUL-1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE OT CAPPA CHAIN V-III REGION (PC 6684). MOS MOSCULUS (MOUSE). EUTHERIA; RODENTIA. [1] SEQUENCE. [
KV3R MOUSE STANDARD; PRT; 111 AA. FOLGTO: 21-JUL-1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE) 10-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE) 10-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE) 10 G KARPA CHAIN V-III RECION (PC 6684). MUS MUSCULUS (MOUSE). EUTHERIA; RODENTIA. [1] EUTHERIA; RODENTIA. [1] EUTHERIA; RODENTIA. [1] FORMANOTICERT M., CATMAITAN L., LOH E., SCHILLING J., HOOD L.E.; NATURE 276:785-790(1978). PIR, A01936; KVMS84. HSSP; PO1679; LACY. IMMUNOCIOBULIN V RECION. DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1. DOMAIN 24 38 COMPLEMENTRRITY-DETERMINING 2. DOMAIN 39 53 FRAMEWORK 2. DOMAIN 54 60 COMPLEMENTRRITY-DETERMINING 2. DOMAIN 61 92 FRAMEWORK 4. DOMAIN 61 92 COMPLEMENTRRITY-DETERMINING 3. DOMAIN 102 111 FRAMEWORK 4. DISULEID 23 92 BY SIMILARITY. NON TER 111 111 SEQUENCE 111 AA; 12039 MM; 66692 CN; MAICHE SIMILARITY 96.4%; Pred. No. 1.74e-140; Matches 107; CONSETVAHINYQKNEGOPRELLIYLASNIES 80 1 divltqspaslavslqqratiscrasksvstsgysymhwyqqkpqqppklliylasnles 60 HillillIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	KUJR MOUSE STANDARD; PRT; 111 AA. FOLGÎO: 21-JUL-1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 10.COT-1993 (REL. 27, LAST SEQUENCE UPDATE) 10.COT-1993 (REL. 27, LAST SEQUENCE UPDATE) 10.COT-1993 (REL. 27, LAST ANNOTATION UPDATE) 10.COT-1993 (REL. 27, LAST ANNOTATION UPDATE) 11. SEQUENCE. 12. SEQUENCE. 13. SEQUENCE. 14. SEQUENCE. 14. SEQUENCE. 15. FRAMINORIA J., LOH E., SCHILLING J., HOOD L.E.; 16. RAPA AND AND AND AND AND AND AND AND AND AN	KUJR MOUSE STANDARD; PRT; 111 P. P01670; 21-JUL-1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; EUTHRIA; RODENTIA. [1] SEQUENCE. 79073152 WEIGER W., CATMAITAN L., LOH E., SCHILLIN NATURE 276:785-790 (1978). PIR; Å01938; KVMS84. WEMPROCIORITIN U. PESTON	KV3R MOUSE STANDARD; PRT; 111 P P01670; 21-JUL-1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE OT KAPPA CHAIN VII REGION (PC 6684). MUS MUS MUSCULUS (MOUSE). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; EUTHERIA; RODENTIA. [1] SEQUENCE. 79073152 MEIGERT M., GATMAITAN L., LOH E., SCHILLIN NATURE 276:785-790 (1978). PIR; À01938; KVMS84.
121 TFGGCTKLEIK 131 SULT 3 KV3R MOUSE STANDARD; PRT; 111 AA. POLSTO; 21-JUL-1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE) 15 EUTRARY METCHT N. GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.; 19073152 19073152 1918, A01938; KVMS84. 11	121 TFCGGTKLETK 131 SULT 3 KV3R MOUSE STANDARD; PRT; 111 AA. P01670; 21—701—1986 (REL. 01, CREATED) 21—701—1986 (REL. 01, LAST SEQUENCE UPDATE) 01—6CT—1993 (REL. 27, LAST ANNOTATION UPDATE) 01—7073152 01—7073153 01—7073154 01—7073154 01—7073154 01—7073154 01—7073155 01—7073155 01—7073157 01—707317 0	121 TFGGCTKLEIK 131 SULT 3 SULT 3 SULC 3 SUCC 3 SUCC 3 SUCC 3 SUCC 4 SUCC 4 SUCC 4 SUCC 5 S	121 TFGGCTKLEIK 131 SULT 3 KV3R MOUSE STANDARD; PRT; 111 AP POLGTO; 21-JUL-1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE OI OCT-1993 (REL. 27, LAST ANNOTATION UPDA IG KAPPA CHAIN V-III REGION (PC 6684). MUS MUSCULUS (MOUSE). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; EUTHRIA; RODENTIA. [1] SEQUENCE. 79973152 WEIGERT M., GATMAITAN L., LOH E., SCHILLIN NATURE 276:785-790 (1978). PIR; À01938; KVMS84.
121 tfgsqtkleik 131 121 TFGGCTKLEIK 131 121 TFGGCTKLEIK 131 121 TFGGCTKLEIK 131 KV3R MUUE ENABARD EUGTO, 12 -00L-1986 (REL. 01, CREATED) 21-00L-1986 (REL. 01, LAST SEQUENCE UPDATE) 13 -00L-1986 (REL. 01, LAST SEQUENCE UPDATE) 14 CKAPPA CHAIN V-III REGION (PC 6684). MUS MUSCULUS (MOUSE). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; [1] SEQUENCE. [1] SEQUENCE. [2] WEIGERT M., CATWAITAN L., LOH E., SCHILLING J., HOOD L.E.; NATURE 276:785-790(1978). PIR, MO1938; KVMSS4. HSSP; P01679; LACY. IMMONICIBELLY REGION. DOMAIN 1 23 COMPLEMENTARITY-DETERMINING 1. DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 2. DOMAIN 39 53 FRAMEWORK 2. DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2. DOMAIN 61 92 FRAMEWORK 3. DOMAIN 61 92 FRAMEWORK 4. DOMAIN 61 92 FRAMEWORK 4. DOMAIN 102 111 FRAMEWORK 4. DOMAIN 103 111 FRAMEWORK 4. DOMAIN 104 111, 111 111 SEQUENCE 111 AA; 12039 MM; 66692 CN; MAICHER 111 111 111 SEQUENCE 111 AA; 12039 MM; 66692 CN; ALCONSTINATION 1 1 MISMATCHES 3; Indels 0; Gaps 1 divltqspaslavslggtatiscrasksvstsgysymhwyqqkpgqppkiliylasnles 60 1 divltqspaslavslggtatiscrasksvstsgysymhwyqqkpgqppkiliylasnles 60 1 lilililililililililililililililililili	121 tfgsqtkleik 131 121 TFGGCTKLEIK 131 121 TFGGCTKLEIK 131 121 TFGGCTKLEIK 131 KV3R WOUSE STANDARD; PRT; 111 AA. P01670; 21-JUL-1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 01-OCT-1933 (REL. 27, LAST ANNOTATION UPDATE) 1G KAPPA CHAIN V-111 REGION (PC 6684). MUS MUSCULUS (MOUSE). EUTHERIA; RODENTIA. [1] EUTHERIA; RODENTIA. [1] EXAMANOTE. [1] SSQUENCE. [1] SSQUENCE. [2] PO1336; KW4S84. [3] COMPLEMENTARITY-DETERMINING 1. [3] POMAIN 1 23 COMPLEMENTARITY-DETERMINING 2. [4] DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 2. [5] DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 3. [6] DOMAIN 102 111 FRAMEWORK 2. [6] DOMAIN 102 111 FRAMEWORK 4. [6] PRAMEWORK 4. [6] PRAMEWORK 4. [6] PRAMEWORK 4. [7] DOMAIN 102 111 FRAMEWORK 4. [8] STAILARITY. [8] SCOURCE 111 AA; 12039 WW; 66692 CN; [8] SCOURT MACHOR 1111; [8] SCOURCE 111 AA; 12039 WW; 66692 CN; [8] Idivitqspasiavslqqratiscrasksystsqysymhwqqkpqqppkliylasnles 60 [1] Illillillillillillillillillillillillilli	121 tfgsgtkleik 131 121 TFGGTKLEIK 131 121 TFGGTKLEIK 131 121 TFGGTKLEIK 131 KV3R MOUSE STANDARD; PRT; 111 AP POL670; 21-JUL-1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE 01-0CT-1993 (REL. 27, LAST ANNOTATION UPDATE 01-0CT-1993 (REL. 27, LAST ANNOTATION UPDATE UTWARYOTA; METAZOA; CHORDATA; VERTEBRATA; EUTHERIA; RODENTIA. 11 12	121 tfgsgtkleik 131 121 TFGGTKLEIK 131 121 TFGGTKLEIK 131 121 TFGGTKLEIK 131 KV3R MOUSE STANDARD; PRT; 111 PPG1670; 21-JUL-1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE GRAPA CHAIN V-III REGION (PC 6684). MUS MUSCULUS (MOUSE). EUTHRIA; RODENTIA. [1] SEQUENCE. 79073152 WEIGERT M., GATMAITAN L., LOH E., SCHILLIN NATURE 276:785-790(1978). PIR; À01938; KVMS84.
61 QQKGQCYELIYLASNLESGVPARFSGSGSCTFTLAITHPUTEEDAATTYCCHSRENTY 120 121 tfgsgtkleik 131 121 TFGGCTKLEIK 131 121 TFGGCTKLEIK 131 122 TFGGCTKLEIK 131 123 KV3R WOUSE STANDARD; PRT; 111 AA. P01670; 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 32 JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 32 JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 32 JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 33 CARANOVATION UPDATE) 34 GARANITAA. 35 JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 3973152 WEIGRAYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; 3973152 WEIGRAYOTA, METAZOA; COMPLEMENTRITY-DETERMINING 1. DOMAIN 24 38 COMPLEMENTRITY-DETERMINING 2. DOMAIN 24 50 COMPLEMENTRITY-DETERMINING 3. DOMAIN 35 53 FRAMENORK 4. DOMAIN 61 92 FRAMENORK 4. DOMAIN 102 111 AP 12039 MM; 66692 CN; DOMAIN 102 111 AP 12039 MM; 66692 CN; MACHOR 111 AA; 12039 MM; 66692 CN; MACHOR 111 AA; 12039 MM; 66692 CN; MACHOR 111 III III SEQUENCE 111 AA; 12039 MM; 66692 CN; MACHOR 107; CONSELVATIVE 1; MIGMATCHER 3; Indels 0; Gaps 1 divltqspaslavslqratiscrasksvetsgysymhwyqdkpdppklliylasnles 60 1 divltqspaslavslqratiscrasksvetsgysymhwyqdkpdppklliylasnles 60 1 lillillillillillillillillillillillillil	61 QCRCGTRELITIASNLESGVPARESGSGSCTDFTLAIHPVEEDAATYTCQHSRENPY 120 121 IfGGTKLEIK 131 121 TFGGGTKLEIK 131 122 TFGGGTKLEIK 131 123 TFGGGTKLEIK 131 123 TFGGGTKLEIK 131 124 TFG TAPPA CHAIN V-III REGION (PC 6684). WIS MUSCULUS (MOUSE). EUTHER A. MCTALLON (PC 6684). BUTARAPOTA; MCTALOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERTA; RODENTIA. SEQUENCE. 19073152 19073152 19073152 19073152 19073152 19073152 19073153 19073154 19073154 19073157 1907317	61 QQRCGOTRILITIASNLESGVPARFSGSGSCTDFTLAIHPVEEDAATTYCQHSRENPY 121 tfgsgtkleik 131 121 TFGGCTRLEIK 131 121 TFGGCTRLEIK 131 121 TFGCTRLEIK 131 121 TFGCTRLEIK 131 121 TFGCTRLEIK 131 122 TFGCTRLEIK 131 123 KV3R MOUSE STANDARD; PRT; 111 AA. P01670; 12-JUL-1986 (REL. 01, CREATED) 13-JUL-1986 (REL. 27) LAST SEQUENCE UPDATE) 10-CT-1993 (REL. 27) LAST SEQUENCE UPDATE) 10-CT-1993 (REL. 27) LAST SEQUENCE UPDATE) 11-CT-1993 (REL. 27) LAST ANNOTATION UPDATE) 11-CT-1993 (REL. 27) LAST ANNOTATION UPDATE) 12-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 13-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 14-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 15-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 16-JUL-1986 (REL. 01, CREATED) 17-JUL-1986 (REL. 01, CREATED) 18-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 19-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE) 19-JUL-1986 (REL. 01, LAST ANDOTATION UPDATE) 19-JUL-1986 (REL. 01, LAST	61 QQRCGOTRILIANGESCVPARFSCSCSCIDETLAIHPVEEDAATYTCOHSRENPY 121 tG99tkleik 131 121 TFGGCTRLEIK 131 121 TFGGCTRLEIK 131 121 TFGCTRLEIK 131 121 TFGCTRLEIK 131 122 TFGCTRLEIK 131 123 KV3R MOUSE STANDARD; PRT; 111 AA. P01670; 21-JUL-1986 (REL. 01, CAFATED) 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE) 1G KAPPA CHAIN V-111 REGION (PC 6684). MUS MUSCULUS (MOUSE). EUTHERIA; RODENTIA. 11 SEQUENCE. 13073152 HEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.; NATURE 276: 785-790 (1978). PIR; A01938; KVMS84.
61 zzkpgzppklliyrasnlzsgiparfsgagsrtbffltibpvzabdvatyfczzsbzbpw 120 112 tfgsgtkleik 131 121 tfgsgtkleik 131 121 tfgsgtkleik 131 121 TFGGGTKLEIK 131 122 TFGGGTKLEIK 131 123 TFGGGTKLEIK 131 124 TFGGGTKLEIK 131 125 TFGGGTKLEIK 131 126 (REL. 01, CREATED) 12-UUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 12-UUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 13-UUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 14-UUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 15-UUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 16-UUL-1986 (REL. 01, LAST SEQUENCE) 17-UUL-1986 (REL. 01, LAST SEQUENCE) 18-UUL-1986 (REL. 01, LAST SEQUENCE) 19-UUL-1986 (REL. 02,	61 zzkpgzppklliyrasnlzsgiparfsgagsrtbffltibpvzabdvatyfczzsbzbpw 120 11 tfgsgtkleik 131 12 tfgsgtkleik 131 13 kv3R MOUSE 10-COT-1993 (REL. 01, LAST SEQUENCE UPDATE) 12 -UUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 12 -UUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 13 tfgstkarvora, METAZOA; CHORDATA, VERTEBRATA; TETRAPODA; MAMMALIA; 14 tfgstkarvora, METAZOA; CHORDATA, VERTEBRATA; TETRAPODA; MAMMALIA; 15 tfgstkarvora, METAZOA; CHORDATA, VERTEBRATA; TETRAPODA; MAMMALIA; 16 tfgstkarvora, METAZOA; CHORDATA, VERTEBRATA; TETRAPODA; MAMMALIA; 17 tfgstgtkarvora, METAZOA; CHORDATA, VERTEBRATA; TETRAPODA; MAMMALIA; 18 tfgstgtkarvora, METAZOA; CHORDATA, VERTEBRATA; TETRAPODA; MAMMALIA; 17 tfgstgtkarvora, MATAZOA; CHORDATA, VERTEBRATA; TETRAPODA; MAMMALIA; 18 tfgstgtkarvora, METAZOA; CHORDATA, VERTEBRATA; TETRAPODA; MAMMALIA; 18 tfgstgtkarvora, MATAZOA; CHORDATA, VERTEBRATA, TETRAPODA; MATAZOA; CHORDATA, MATAZOA; M	61 zzkpgzppklliyraenlzegiparfeggsrtbftltibpvzabdvatyfczzsbzbpw :: :	61 zzkpgzppklliyraenlzegiparfeggsgrtbftltibpvzabdvatyfczzsbzby :: : :
	1 MESDTLILMYLLIAWPGSTGDITLIGGRESSIGNYCHARMY 60 51 ZZKPGZPDLILIAWLLIAWPGSTGDITLIGGRESSIGNYCHARMY 120 51 ZZKPGZPDLILIAWLLIAWPGSTGDITLIGGRESSIGNYCHARMY 120 51 STRINDARL 11 STRINDARD 120 51 LTGGGTKLEIK 131 51 TFGGGTKLEIK 131 52 TFGGGTKLEIK 131 53 FKV3R MOUSE STANDARD; PRT; 111 AA. POLGT-1993 (REL. 01, CREATED) 51 -UJL-1986 (REL. 01, CREATED) 52 -UJL-1986 (REL. 01, LAST SEQUENCE UPDATE) 53 SEQUENCE 10 COCKPORTIAN V-11 REGION (PC 6684). 54 MUS MUSCOLUS (MOUSE). 55 SEQUENCE 10 COCKPORTIAN 1 SEGUENCE UPDATE) 67 KAPPA CHAIN V-111 REGION (PC 6684). 68 MUS MUSCOLUS (MOUSE). 68 SEQUENCE 10 COMPLEMENTARITY-DETERMINING 1. 69 SEQUENCE 10 COMPLEMENTARITY-DETERMINING 2. 60 DOMAIN 1 2 3 COMPLEMENTARITY-DETERMINING 3. 60 COMPLEMENTARITY DETERMINING 3. 60 SEAMENORK 3. 60 COMPLEMENTARITY DETERMINING 3. 60 SEAMENORK 4. 61 92 FRAMENORK 4. 61 92 FRAMENORK 4. 66 OCCUPLEMENTARITY-DETERMINING 3. 60 COMPLEMENTARITY DETERMINING 3. 60 SEAMENORK 4. 61 92 BY SIMILARITY. 66 SEPAMENORK 4. 67 DOMAIN 61 92 BY SIMILARITY. 68 SEQUENCE 111 AA; 12039 MM; 66692 CN; 66692 CN; 66 COCKPLEMENTARITY DETERMINING 9. 68 SEQUENCE 111 AA; 12039 MM; 66692 CN; 6661 LOCAL SIMILARITY 96.4%; PREG. NO. 1.14e=140; 68 SEQUENCE 111 AA; 12039 MM; 66692 CN; 68 SECUENCE 111 MM; 111 HILLIN HILLIH HILL	1 INTELLIMENTALIAMPEGSTCDIVITOSPASIGNSTRICTERINING INTELLIMENTALIAMPEGSTCDIVITOSPASIGNSTRICTERINING INTELLIMENTALIAMPEGSTCDIVITOSPASIGNSTRISTERINING INTELLIMENTALIAMPEGSTCDIVITOSPASIGNSTRISTERINING INTELLIMENTALIAMPEGSTCD INTELLIMENTALIAMPEGSTCO INTERNATION INTERNATION INTELLIMENTALIAMPEGSTCO INTERNATION INTERNATION INTELLIMENTALIAMPEGSTCO INTERNATION	1 INTELLIMPLE STREET ST
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Jactobes 101, Conservative 20; Mismatches 10; Indels 0; Gaps 1 metdelllwillwygstgdivitgepsalsviggratiscrasksnrygnsfarwy 60 metdelllwillwygstgdivitgepsalsviggratiscrasksnrygnsfarwy 60 metdelllwillwygstgdivitgepsalsviggratiscrasksnrygnsfarwy 60 metdelllwillwygstgdivitgepsalsviggratiscrasksnrygnsfarwy 60 metdelllwilllwillwygstgdivitgepsalsviggratiscrasksnrygnsfarwy 60 metdelllwillwindwygstgdivitgepsalsviggratiscrasksnrygnsfarwy 60 metdellwillwygstgdivitgepsalsviggratiscrasksnrygnsfarwy 60 metaphillyrasnlzsgiparfsgsgstdfftliplill	datches 10cal Similarity 71.1%; Fred. Ro. 1.50e-103; Fred. Conservative 71.1%; Fred. Ro. 1.50e-103; Fred. Ro. 1.50	Jacches Jamisarry 17.18; Fred. No. 1.136=133; Adtches 10; Conservative 20; Mismatches 10; Indels 0; Gaps 1 metdilluvilluvpgstgdivltgspaslavslggratiscrasksvntygnsfmzwy 60 [1:1	Jacches Jamisarry 17.18; Fred. No. 1.136=133; Atches 10; Conservative 20; Mismatches 10; Indels 0; Gaps I metdilluvilluvpgstgdivltgspaslavslggratiscrasksvntygnsfmzwy 60
Duery Match Best Local Similarity 77.1%; Pred. No. 1.36e-155, datches 101; Conservative 20; Mismatches 10; Indels 0; Gaps 1 metdtillwillwypgstgddivitgapaslavslggratiscraskavitygnsfmzwg 60 1 metdtillwillwypgstgddivitgapaslavslggratiscraskavitygnsfmzwg 60 1 metdtillwillwypgstgddivitgapaslavslggratiscraskavitygnsfmzwg 60 1 metdtillwillwypgstgdivitgapaslavslggratiscraskavitygnsfmzwg 60 1 metdtillwylliwypgstgdivitgapaslavslggratiscraskavitygnsfmzwg 60 1 metdtillwylliwypgstgdivitgapaslavslggratiscraskavitygnsfmzwg 60 1 metdtillwylliwypgstgdivitgapaslavslggratiscraskavitygnsfmzwg 60 1 mesdfillwylliwypgstgdivitgapaslavslggratiscraskavitygnsfmzwg 61 1 mesdfillwylliwypgstgdivitgapaslavslggratiscraskavitygnsfmzwg 61 1 tigsgtkleik 131 1 1 1 1 1 1 1 1 1	Deet Match Best Local Similarity 77.1%; Pred. No. 1.36e-155; datches 101; Conservative 20; Mismatches 10; Indels 0; Gaps 1 metdtillwipstdivitgapalavsiggtatiscraskswrtygnsfmzwy 60	BS.6%; Score 806; DB 4; Length 132;	Duery Match 85.6%; Score 806; DB 4; Length 132; Best Local Similarity 77.1%; Pred. No. 1.36e-155, Aatches 101; Conservative 20; Mismatches 10; Indels 0; Gaps 1 metdillwullwvpgstgdivltgspaslavslggratiscrasksvntygnsfmzwy 60 :
NOW TER	NOW_TER	NOW TER 132 AA; 14523 MW; 114870 CN; SEQÜENCE 132 AA; 14523 MW; 114870 CN; SUBTION TER 132; Sext Local Similarity 77.1%; Pred. No. 1.36e-155; Sext Local Similarity 77.1%; Pred. No. 1.36e-155; Sext Local Similarity 77.1%; Pred. No. 1.36e-155; Adtches 101; Conservative 20; Mismatches 10; Indels 0; Gaps 1 metdilluvilluvygstgdivltgspaslavslggratiscrasksvntygnsfmzwy 60 11:1111111111111111111111111111111111	NON TERE 132 132 132 132 NON TERE 132 132 132 134 135: SEQÜENCE 132 Aa; 14523 MW; 114870 CN; Sest Local Similarity 77.1%; Pred. No. 1.36e-155; Sest Local Similarity 77.1%; Pred. No. 1.36e-155; Set Local Similarity 77.1%; Pred. No. 1.36e-155; Imeddilluvilluvvpgstgdivltgspaslavslggratiscrasksvntygnsfmzwy 60 Imeddilluvilluvvpgstgdivltgspaslavslggratiscrasksvntygnsfmzwy 60 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
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FT DOMAIN 61 92 FRAMEWORK 3. FT DOMAIN 93 101 COMPLEMENTY-BETERNINING 3.	DOMIN 102 111 DISULFID 23 92 NON TEP 111 111	ď,	Query Match 77.0%; Score 725; DB 4; Length 111; Best Local Similarity 93.7%; Pred. No. 8.86e-137; Matches 104; Conservative 2; Mismatches 5; Indels 0;	Db 1 divltgspaslavslggratiscrasksvsafgysymhwygdkpgqppklliylasnles 	Db 61 gvparfsgsgsgtdftlnihpveeedavtyvcqhsrelpptfgggtkleik 111 	SULT	ID KV3U MOUSE STANDARD; PRT; 111 AA. AC P01673;			OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; OC EUTHERIA; RODENTIA. DN 11)	0;	RA RA RL -	S C C C C C C C C C C C C C C C C C C C	IMMUNOGLOBULI DOMAIN DOMAIN	DOMAIN 24 38 DOMAIN 39 53 DOMAIN 54 60	DOMAIN 61 92 FRAMEWORK 3.	DOMAIN 102 111	DISULFID 23 92 BY NON TER 111 111	SQ SEQUENCE III AA; II986 MW; 66852 CN;
RESULT 4 ID KV38 MOUSE STANDARD; PRT; 111 AA.	(REL. 01, CREATED)			RP SEQUENCE. RM 79073152 RM 79073154 WEIGERT M., GATWAITAN L., LOH E., SCHILLING J., HOOD L.E.;	NATURE 216: 182-190 (1918). PIR; B01938; KVMS75. HSSP; P01679; 1ACY. IMMUNOGLOBULIN V REGION.	DOMAIN 1 23 DOMAIN 24 38 DOMAIN 39 53	FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2. FT DOMAIN 61 92 FRAMEWORK 3.	FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3. FT DOMAIN 102 111 FRAMEWORK 4. FT DISULFID 23 92 BY SIMILARITY.	FT NON TER 111 111 SQ SEQUENCE 111 AA; 12010 MM; 66974 CN;	Query Match 77.94; Score 734; DB 4; Length 111; Rest Local Similarity 94 68: Pred. No. 7.28=130:	vative	Db 1 divltgspaslavslggratiscrasksvategysymhwygdkpgqppklliylasnles 60	21 DIVILYSTADEGVERGYRALISCRASNAVSISGISIRMMIKKRYGVEGYFREELILHANDES 61 gvparfsggsgtdftlnihpveeedaatyycqhsrelpltfgagtklelk 111	Qy 81 GVPARFSGSGSGTDFTLNIHPVEEEDAATYYCQHSRENPYTFGGGTKLEIK 131	RESULT 5	ID KV3T MOUSE STANDARD; PRT; 111 AA.			DE IG MAY'R CHAIN V-111 KEGION (PC /940). OS MUS MUSCULUS (MOUSE).

ö 1 divltqspaslavslgqratiscrasksvstsgysymhwyqqkpgqppklliylassles 60 21 DIVLIGSPASLGVSLGQRATISCRASKSVSTSGYSYMHWYQQKPGQTPKLLIYLASNLES 80 Gaps CULUS (MOUSE). TA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; ö COMPLEMENTARITY-DETERMINING 1. M., GATWAITAN I., IOH E., SCHILLING J., HOOD L.E.; 276:785-790(1978).
PC 4285 AND PC 4039 SEQUENCES ARE IDENTICAL. COMPLEMENTARITY-DETERMINING 2. COMPLEMENTARITY-DETERMINING 3. 76.4%; Score 720; DB 4; Length 111; 91.9%; Pred. No. 1.27e-135; 4; Indels 1986 (REL. 01, CREATED)
1986 (REL. 01, LAST SEQUENCE UPDATE)
1993 (REL. 27, LAST ANNOTATION UPDATE)
1A CHAIN V-III REGION (PC 2485 AND PC 4039). 5; Mismatches 111 AA BY SIMILARITY. FRAMEWORK 4. FRAMEWORK 2. FRAMEWORK 3. FRAMEWORK 1. 11986 MW; 66852 CN; 1 Similarity 91.9%; 102; Conservative STANDARD; 01679; 1ACY. 23 38 53 60 60 92 101 111 111 1939; KVMS85. Best Local Similarity 111 AA; A; RODENTIA. DISULFID NON TER SEQUENCE Query Match DOMAIN DOMAIN DOMAIN Matches 61 SELLLLES 염 g à

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19073152 WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.; NATURE 276:785-790(1978).

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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; COMPLEMENTARITY-DETERMINING 1. COMPLEMENTARITY-DETERMINING 1. COMPLEMENTARITY-DETERMINING 3. WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.; NATURE 276:785-790(1978). PIR; D01937; KVMS10. HSSP; P01679; 1GGB. Query Match 69.6%; Score 656; DB 4; Length 111; Best Local Similarity 83.8%; Pred. No. 7.58e-121; Matches 93; Conservative 9; Mismatches 9; Indels 68.9%; Score 649; DB 4; Length 110; 83.8%; Pred. No. 3.10e-119; COMPLEMENTARITY-DETERMINING Indels COMPLEMENTARITY-DETERMINING COMPLEMENTARITY-DETERMINING æ 21-JUL-1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE) IG KAPPA CHAIN V-III REGION (PC 7210). 9; Mismatches 110 AA BY SIMILARITY BY SIMILARITY FRAMEWORK 4. FRAMEWORK 1. FRAMEWORK 2. FRAMEWORK 3. FRAMEWORK 1. FRAMEWORK 4. 11950 MW; 65304 CN; 65935 CN; FRAMEWORK FRAMEWORK PRT; 12011 MW; 93; Conservative STANDARD; NATURE 276:785-790(1978) IMMUNOCLOBULIN V REGION 23 38 53 60 60 92 110 92 IMMUNOGLOBULIN V REGION 23 38 53 60 60 92 111 92 MUS MUSCULUS (MOUSE). PIR; E01937; KVMS69. Best Local Similarity 111 AA; EUTHERIA; RODENTIA. 110 AA; HSSP; P01679; 1ACY 24 39 54 61 61 93 23 KV3P MOUSE SEQUENCE. DISULFID SEQUENCE Query Match DISULFID SEQUENCE 79073152 NON TER 15 P01668; DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN NON TER DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN Matches 음 ð 용 g ð à ö 1 divltqspaslavslgqratisckasqsvdydgdsymnwyqqkpgqppklliyaasnles 60 1 DIVIJQSPASLGVSLGQRATISCRASKSVSTSGYSYMHWYQQKPQPRLLIYIASNLES 80 80 Gaps 21 DIVLIQSPASLGVSLGQRATISCRASKSVSTSGYSYMHWYQQKPGQTPKLLIYLASNLES ö EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; 61 giparfsgsgsrtdftltinpveaddvatyycqqsnedpytfgggtkleik 111 COMPLEMENTARITY-DETERMINING 1. COMPLEMENTARITY-DETERMINING 2. 'n WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.; LOH E., SCHILLING J., HOOD L.E.; Score 660; DB 4; Length 111; 9; Indels COMPLEMENTARITY-DETERMINING Pred. No. 9.10e-122; LAST SEQUENCE UPDATE), LAST ANNOTATION UPDATE) 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE) 8; Mismatches 111 AA 111 AA BY SIMILARITY. FRAMEWORK 3. FRAMEWORK 4. FRAMEWORK 1. FRAMEWORK 2. MW; 63600 CN; IG KAPPA CHAIN V-III REGION (PC 7183) IG KAPPA CHAIN V-III REGION (PC 7769) PRT; PRT; KV3Q MOUSE STANDARD; F P01669; 21-JUL-1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 01, CREATED) Query Match 70.1%; Best Local Similarity 84.7%; 11952 WEIGERT M., GATMAITAN L., NATURE 276:785-790(1978). 94; Conservative STANDARD; PIR; B01937; KVMS83. HSSP; P01679; 1GGB. IMMUNOGLOBULIN V REGION. 23 38 53 60 60 92 101 1111 MUS MUSCULUS (MOUSE). MUS MUSCULUS (MOUSE). 01-0CT-1993 (REL. 27 21-JUL-1986 (REL. 01 EUTHERIA; RODENTIA EUTHERIA; RODENTIA.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Run on:

Mon Jul 8 08:29:02 1996, MasPar time 4.45 Seconds 243.853 Million cell updates/sec

Tabular output not generated.

>US-08-137-117B-25 (1-131) from US08137117B.pep 942 1 MESDTLLIMVLLIMVPGSTG.......CQHSRENPYTFGGGTKLEIK 131 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

70887 seqs, 8282111 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq22 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14

Mean 30.229; Variance 161.993; scale 0.187 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	1.32e-63	1.96e-56	6.43e-54								6.50e-50	4.73e-49
	Description	p12-k2.	Anti-idiotype antibod	Mouse MAb 3B9 light c	Amino acids sequence	Anti-idiotype antibod	Anti-CD4 antibody MT	Anti-Leu 3a light cha	p64-k4 protein produc	kappa light chain var	Antibody 4A2 light ch	Light chain variable	Mouse 4C10 anti-idiot
	O	R28668	R74967	R70189	P90543	R74966	R32123	R04132	R29008	R10920	R30881	R05089	R37716
	DB	9	14	13	-	14	9	-	9	m	9	П	~
	luery Match Length DB	131	130	132	131	146	131	131	131	132	131	131	132
œ	Query Match	100.0	90.3	86.9	9.98	85.9	85.5	84.6	83.4	83.3	82.9	81.5	80.4
	Score	942	851	819	816	808	802	797	786	785	781	168	757
	Result No.	-	2	c	4	5	9	7	œ	6	10	11	12

1.52e-46 7.70e-46	4.67e-45 9.59e-45	1.15e-44	2.82e-44	5.80e-44	1.43e - 43	2.04e - 43	2.04e-43	2.45e-43	2.93e-43	2.53e-42	2.53e-42	1.07e-41	1.10e - 40	1.32e-40	2.26e-40	3.23e-40	4.63e-40	6.63e-40	1.14e - 39	1.63e - 39	m	m		3.99e - 39	4.77e-39	6.83e-39	6.83e-39	6.83e-39	8.17e-39	4.10e-38
Vl region from an ant Anti-carcinoembryonic	N-terminal sequence o Porphyrin antibody li	n var		Immunoglobulin light		Mouse antibody F4-7 l	Mouse antibody FB3-2	Light chain variable		Mouse anti-HIV mu5.5	Anti HIV antibody lig	Immunoglobulin L chai	Human IgE receptor-bi	Human IgE receptor-bi	MaE11 light chain.	Murine NM-01 variable	Murine anti-CD18 Ab 6	Chimeric MAb 9.2.27 1	Light chain variable	Murine 1B4 light chai	Sequence of the monoc		Anti-Tac light chain	Humanised anti-Tac an	MaE15 light chain.	Immunoglobulin light	Anti-idiotype antibod	Sequence of the monoc	of the]	Sequence of the light
R80272 R60564	R07456 R52659	R15442	R74956	R74957	R75431	R75459	R75457	R60528	R15440	R55123	R60302	P90541	R79156	R79158	R33305	R65172	R47494	R10539	R60810	R13089	R48615	R33346	R06375	R24108	R33309	R74955	R74965	R48618	R59511	R48620
	112 2 212 10	•	110 14	-	112 14	218 14	218 14	111 11	125 3		111 111	111	112 14	112 14		111 13	111 9	112 2	110 10	112 3	121 9	121 6		126 2		112 14	118 14	120 9	133 10	120 9
77.0	74.9		73.9	73.5	72.9	72.7	72.7	72.6	72.5	71.2	71.2	70.4	0.69	6.89	9.89	68.4	68.2	6.79	9.19	67.4	67.1	0.79	6.99	6.99	8.99	9.99	9.99	9.99	66.5	65.5
725 716	706	701	969	692	687	685	685	684	683	671	671	663	650	649	949	644	642	640	637	635	632	631	630	630	679	627	627	627	979	617
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p12-h2.

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61 QQKPGQTPKLLIYLASNLESCVPARFSGSGSGTDFTLNIHPVEEEDAATYYCQHSRENPY 120

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Spleen cells from mice immunized with human IL-4 were used to prepare hybridomas, which were screened for anti-IL-4 MAb secretion. Only 61 qqkpqqppklliyaasnlesgiparf6qsqsqtdftlnihpveeedaatyycqqsnedpp 120 61 QOKPGQTPKLLIYLASNLESGVPARFSGSGSGTDFTLNIHPVEEEDAATYYCQHSRENPY 120 1 metdtillwvlllwvpgstgdivltqspaslavslggratisckasgsvdydgdsymnwy 60 1 MESDILLIMVLLLMVPGSTGDIVLTQSPASLGVSLGQRATISCRASKSVSTSGYSYMHWY Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived clone 3B9 was positive. cDNA clones of the 3B9 light and heavy chains were cloned into pGEM7f+ and transformed into E. coli DH5-alpha. The clones were sequenced (Q83490-91), and used for antibody engineering. from high affinity mAbs - useful in treatment of IL-4-mediated Chimeric antibody; humanized antibody; antibody engineering; Score 819; DB 13; Length 132; Pred. No. 6.43e-54; 8; Mismatches 9; Indels monoclonal antibody; MAb; interleukin-4; IL-4; allergy /note= "complementarity determining region" /note= "complementarity determining region" 'note= "complementarity determining region" and IgE-mediated allergic conditions Holmes SD, Sylvester DR; Location/Qualifiers Disclosure; Fig.1; 97pp; English. JT 3 R70189 standard; Protein; 132 AA. (SMIK) SMITHKLINE BEECHAM CORP. (SMIK) SMITHKLINE BEECHAM PLC. Query Match 86.9%; Best Local Similarity 87.0%; 20-SEP-1995 (first entry) 114; Conservative Mouse MAb 3B9 light chain. 113..121 07-SEP-1993; US-117366. 44..58 14-0CT-1993; US-136783 1..20121 TFGGGTKLEIK 131 121 tfgggtkleik 131 121 TFGGTKLEIK 131 07-SEP-1994; U10308. /label= Sig_peptide Gross MS, Holmes S WPI; 95-123387/16. N-PSDB; 083490 WO9507301-A 16-MAR-1995. /label= CDR /label= CDR /label= CDR Sequence Peptide R70189; Mus sp. Region Region Region Matches g δ 셤 8 g ð ð 1; Example 5; Page 20; 28pp; Japanese. R74960-R74969 are clones of the anti-idiotype antibodies Idio3, Idio17, Idio20, Idio27 and Idio33 against a human anticancer monoconal antibody. These antibodies and DNA encoding them are useful in pharmacological, ö qqrpgqpprlliylvsnldsgvparfsgsgsgtdftlnihpveeedaatyycqhi-egay 119 $61\ \mathsf{qqkpqqtpklliylasnlesqvparfsqsqsqtdftlnihpveeedaatyycqhsrenpy}\ 120$ 61 QQRPGQTPKLLIYLASNLESGVPARFSGSGSGTDFTLNIHPVEEEDAATYYCQHSRENPY 120 Gaps The sequences given in R28668-69 were encoded by plasmid sequences which were used in example to illustrate the production of a human antibody which recognises human interleukin-6 receptor (IL-6R). The antibody comprises light (L) chain and heavy (H) chain variable regions which were derived from a mouse monoclonal antibody produced from the hybridoma AUK12-20 which contained the plasmids p12-k2 and 1 mesdtlllwvlllwvpgstgdivltqspaslgvslgqratiscrasksvstsgysymhwy 60 1 MESDILLIMVILLMVPGSIGDIVLIQSPASLGVSLGQRATISCRASKSVSISGYSYMHWY 60 0; Gaps Novel anti-idiotype antibody against an human anticancer monoclonal Anti-idiotype antibody Idio20 clone 20KB1. Antibody, cancer; CDR; heavy chain; light chain; immunoglobulin; 6; Indels 1; antibody - and DNA sequences encoding the antibody, useful in Score 851; DB 14; Length 130; Pred. No. 1.96e-56; Length 131; 0; Indels Score 942; DB 6; 1 Pred. No. 1.32e-63; pharmacology, medicine and biochemical fields. 6; Mismatches 0; Mismatches research Location/Qualifiers complementarity determining region. medical and biochemical fields of R74967 standard; Protein; 130 AA. 90.3**%**; 90.1**%**; Query Match 100.0%; Best Local Similarity 100.0%; 02-FEB-1996 (first entry) 118; Conservative 131; Conservative 1..20 /label= signal peptide J07101999-A 06-0CT-1993; JP-272950. 121 tfqqqtkleik 131 121 TFGGGTKLEIK 131 06-0CT-1993; 272950. (HAGI/) HAGIWARA Y. Best Local Similarity WPI; 95-182987/24. Sequence 131 AA; N-PSDB; Q90432.

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R74967;

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Sequence Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 QQKPGQTPKLLIYLASNLESGVPARFSGSGSGTDFTLNIHPVEEEDAATYYCQHSRENPY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 metdtillwvlllwvpgstgdivltqspaslavslggratisckasqsvdydgdsymnwy 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel anti-idiotype antibody against an human anticancer monoclonal antibody - and DNA sequences encoding the antibody, useful in
                                                                                                                                                                                                                                                         Chimeric anti-human immune virus antibodies - contg. mouse variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-idiotype antibody Idiol7 clone 17KB1.
Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;
                                                                                                                                                                                        Tokiyoshi S, Matsushita S, Hattori T,
                                                                                                                                                                                                                                                                        regions and human constant regions for diagnosis, treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                      The sequence from Asp 21 encodes the L chain variable region.
                                                                                                                                                                                                                                                                                                                     The sequence is encoded by a V chi region gene (see N90495)
                                             Amino acids sequence of a V chi region gene.
V cji region; immunoglobulin; L chain variable region; HIV.
                                                                                                                                                                                                                                                                                                                                                                                  Score 816; DB 1; Length 131;
Pred. No. 1.11e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Indels
                                                                                                                                                                        The Chemo-Sero-Therapeutic Research Institute.
Maeda H, Eda Y, Kimachi K, Tokiyoshi S, Matsus
                                                                                                                                                                                                                                                                                                                                                                                                                 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complementarity determining region
                                                                                                                                                                                                                                                                                                    Disclosure; Fig 8; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R74966 standard; Protein; 146 AA.
P90543 standard; protein; 131 AA
                                                                                                                                                                                                                                                                                                                                                                                   Query Match 86.6%;
Best Local Similarity 85.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-FEB-1996 (first entry)
                              20-0CT-1989 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                  112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-0CT-1993; JP-272950.
                                                                                                                                      30-JAN-1988; JP-20255.
08-JUL-1988; JP-171385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= signal peptide
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                                                                                                                         30-JAN-1989; 101583.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HAGI/) HAGIWARA Y.
                                                                                                                                                                                                        Takatsuki K;
WPI; 89-229050/32.
                                                                                                                                                                                                                                                                                         prevention of AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 95-182987/24.
                                                                                                                                                                                                                                                                                                                                                      131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; 090431.
                                                                               Mus muscularis
                                                                                                                                                                                                                                         N-PSDB; N90495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-APR-1995.
                                                                                            EP-327000-A.
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                                                                                                           09-AUG-1989
                                                                                                                                                                                                                                                                                                                                                       Sequence
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1; Example 5; Page 19; 28pp; Japanese. R74960-R74969 are clones of the anti-idiotype antibodies Idio3, Idio17, Idio20, Idio27 and Idio33 against a human anticancer monoconal antibody. prlliylvsnlesgvparfsgsgstdftlnihpveeedaatyycqhir-gaytfgggtk 119 9 8 LMVLLLWVPGSTGDIVLTQSPASLGVSLGQRATISCRASKSVSTSGYSYMHWYQQKPGQT 67 These antibodies and DNA encoding them are useful in pharmacological, Gaps 1 lwvlllwvpgstgdivltqspaslavslgqrasisyrasksvstsgysymhwnqqkpgqp 1; Length 146; 6; Indels US-08-137-117B-25 rag Score 809; DB 14; Pred. No. 3.93e-53; pharmacology, medicine and biochemical fields 4; Mismatches medical and biochemical fields of research 85.9%; 91.1%; Matches 113; Conservative Best Local Similarity 120 leik 123 128 LEIK 131 Sequence Query Match Jul 8 08:19 61 음 F & S S S S S S S 유 8 유 ð ð

inhibiting and when used together their immunosuppressive properties 90090702). The anti-CD4 antibody is used with at least one anti-IL2R immunosuppression; tissue transplantation; graft; L chain; V region; T-helper cell inhibition; transplant rejection; MAb; Synergistic antibody compsn. for use as immunosuppressant - comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R proliferation to effectively inhibit transplant rejection at low doses without significantly reducing the general immune response. See also Q36608-Q36616. anti-CD4 monoclonal antibody for use in the claimed synergistic composition. MAb MT 3.10 is deposited as clone 3.101/sB10 (ECACC alpha or beta antibody. Individually the antibodies are strongly This sequence is the light chain variable region of a preferred are improved; they synergistically inhibit T-helper cell 02-JUN-1993 (first entry) Anti-CD4 antibody MT 3.10 light chain variable region. Weidle U; Kaluza B, Riethmueller G, Scheuer W, WPI; 93-037582/05. alpha- or anti-IL2R beta antibodies Location/Qualifiers JT 6 R32123 standard; Protein; 131 AA. (BOEF) BOEHRINGER MANNHEIM GMBH. Claim 5; Page 11; 18pp; German. 121..131 25-JUL-1991; DE-124759. 30-DEC-1991; DE-143214. interleukin-2 receptor. 1..2030-DEC-1991, 143214. /label= Variable /label= signal N-PSDB; Q36609 02-JUN-1993 28-JAN-1993. DE4143214-A /label= J1 Peptide R32123; Region Region DATA COLOR DE LA COLOR C

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kappa light chain variable region of T84.66 monoclonal antibody. MAb T84.66; kappa light chain; carcinoembryonic antigen; CEA; human adenocarcinoma; mouse-human chimaeric antibody Region 70..80 /label= complementarity determining region /label= complementarity determining region 'label= complementarity determining region /note= "sequenced as peptide fragment" Region 44..57 Location/Qualifiers LT 9 R10920 standard; Protein; 132 AA. Best Local Similarity 82.4%; 08-MAY-1991 (first entry) 108; Conservative Ş 110..121 24-APR-1992; J00544. 25-APR-1991; JP-095476. 19-FEB-1992; JP-032084. (CHUS) CHUGAI SEIYAKU KI 21..131 peptide" /label= tryptic peptide 'note= "Signal peptide" 121 tfgagtklelk 131 |||:|||||:| |121 TFGGGTKLEIK 131 determining regions WPI; 92-398882/48. "Mature N-PSDB; Q3075 Mus musculus. W09219759-A. 12-NOV-1992. Synthetic. Sequence Query Match Peptide Protein Peptide R10920; /note= Region Matches 음 g ò a ð ð ö ö 61 qqkpqqppklliyaasnlesgiparfsgsgsgtdftlnihpveeedaatyycqqssedpp 120 61 QQRPGQTPKLLIXLASNLESGVPARFSGSGSGTDFTLNIHPWFEEDAATYYCQHSRENPY 120 9 9 1 metdtillwvlllwvpgstgdivltqspaslpmslgqratisckasqsldydgdsymnwy 60 1 MESDTLLIMVLLLWVPGSTGDIVLTQSPASLGVSLGQRATISCRASKSVSTSGYSYMHWY 60 Gaps 30-MAR-1993 (first entry) p64-k4 protein product. Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H; Gaps ይ 1 metdtillwvlllwvpgstgdivltqspaslavslggratisckasgsvdydgdsymnwy Claim 1; Fig 2; 12pp; English. Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can used to form chimeric mouse-variable, human-constant region Abs suggested as being useful as a vaccine to HIV. ; 0 ; 0 Anti-Leu 3a light chain variable region gene product, 206 Vx. Score 797; DB 1; Length 131; Pred. No. 3.44e-52; Score 805; DB 6; Length 131; Pred. No. 8.10e-53; 9; Mismatches 10; Indels contg. human antibody regions, and DNA encoding sequences. 9; Indels New chimeric variants of murine antibody anti-leucine -12; Mismatches HIV; AIDS; anti-Leu3A; vaccine; ds. R04132 standard; protein; 131 AA. R29008 standard; Protein; 131 AA. Query Match 84.6%; Best Local Similarity 84.0%; 85.5%; 85.5%; (BECT) Becton Dickinson Co. Hinton R, Oi VT; 06-SEP-1990 (first entry) 110; Conservative 112; Conservative 25-APR-1990. 11-OCT-1989; 010415. 17-OCT-1988; US-260558. 121 tfaggtnleik 131 121 TFGGGTKLEIK 131 121 tfgggtkleik 131 121 TFGGGTKLEIK 131 Query Match Best Local Similarity Matches 112; Conser WPI; 90-126329/17. N-PSDB; Q04039. Mus musculus. Sequence R29008; Matches

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RESULT n SE PP

ö used in example to illustrate the production of a human antibody which recognises human interleukin-6 receptor (IL-6R). The antibody comprises light (L) chain and heavy (H) chain variable regions which were derived from a mouse monoclonal antibody produced from the hybridoma AUK64-7 which contained the plasmids p64-k4 and p64-h2. 1 mesdtlllwvlllwvpgstgdivliqspaslavslggratiscrasesvdsygnsfmhwy 60 Disclosure; Page 124-125; 207pp; Japanese. The sequences given in R29008-09 were encoded by plasmids which were heavy chain; variable region; mouse; monoclonal; hybridoma; AUK64-7; plasmid; p64-k4; p64-h2. 0; Gaps has low antigenicity and contains mouse V-region complementarity Reconstituted human antibody to human interleukin-6 receptor 83.4%; Score 786; DB 6; Length 131; 82.4%; Pred. No. 2.51e-51; 10; Mismatches 13; Indels Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M; Location/Qualifiers 1..20

WO9101990-A 21-FEB-1991

Sequence

7 Matches

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W0922334-A. 23-DEC-1992.

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R30881;

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Sequence Query Match

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Togheter with the heavy chain variable domain (R05090) the sequence forms Light chain variable domain of human chorion gonadotrophin-binding peptd. They also have diagnostic applications as immune reagents for in vivo diagnosis, eg for localisation of tumours and for in vitro diagnosis for detection of hCG in body fluids. 61 QQKPGQTPKLLIYLASNLESGVPARFSGSGSGTDFTLMIHPVEEEDAATYYCQHSRENPY 120 qqkpgqppklliyaasnvesgvparfsgsgsgtdfslnihpvgeediamyfcqqsrkvpw 120 9 9 Human chorionic gonadotropin; antibodies; choriocarcinoma; abortion; Polypeptide(s) which specifically bind human chorionic gonadotropin fragment (FhCG). For the production of Abs the variable region was fused to a constant region of human origin. 1 mesdtlllwvlllwvpgstgdivltqsqaslavslgqratiscrasesveyygtslmqwy The product can be used to prevent pregnancy or for combatting contq. antigen-binding domains comprising complementary determining domains. tumour detection; complementary determining regions; US-08-137-117B-25.rag choriocarcinomas or other hCG-producing tumours. Location/Qualifiers R05089 standard; protein; 131 AA. pregnancyprevention; light chain. Jul 8 08:19 쇰

121 TFGGGTKLEIK 131

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Jul 8 08:19

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VI region from an antibody against cancer-specific mucin.
Antibody; heavy chain; light chain; variable region; cancer; mucin; hybridoma cell; expression vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of cancer cells bearing the gangliosides. It can be used for treating cancers partic. melanomas. It can also be used as an immunomodulator to enhance anti-cancer immunity, suppress organ transplant rejection and suppress autoimmune disease. The MAIA can also be used in the diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 30-31; 46pp; English.
The sequence is that of the 4C10 anti-idiotype Ab light chain V region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 OOKPGOTPKLLIYLASNLESGVPARFSGSGSGTDFTLNIHPVEEEDAATYYCQHSRENP- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 qqkpqqppklliyrasklesgiparfsgsesrtdftltinpveaddvatyycqqsnedpt 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anti-idiotype antibody (MAIA). The MAIA elicits an anti-ganglioside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  response and produces antibodies which induce cytotoxic destruction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 metdtlllwvlllwvpgstgdivltqspaslavslgqratmscrasesvdsyvnsfmhwy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MESDTLLLWVLLLWVPGSTGDIVLTQSPASLGVSLGQRATISCRASKSVSTSGYSYMHWY
                                                                          Mouse 4C10 anti-idiotype Ab light chain V region.

MAIA; monoclonal antibody; hybridoma; organ transplant rejection; immuno-modulator; cancer; treatment; diagnosis; melanoma;
                                                                                                                                                                                                                                                                                                                                                                                                      useful as immuno-modulators for treating and diagnosing cancers, and for suppressing organ transplant rejection and auto:immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          which was used in the construction of a murine/human monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 757; DB 7; Length 132;
Pred. No. 4.73e-49;
                                                                                                                                                                                                                                                                                                                                                                                 Chimeric murine-human anti-idiotype monoclonal antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fv; human; constant domain; chimera; anaphilaxis.
                                                                                                                                        anti-cancer immunity; enhancement; suppression.
                                                                                                                                                                                                                    /note= "Thr -> Ser, from PCR substituted gene"
                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                              Hastings A, Irie RF, Morrison SL.
WPI; 93-182538/22.
                    R37716 standard; Protein; 132 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 80.4%;
Best Local Similarity 79.5%;
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                                                        30-SEP-1993 (first entry)
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12-NOV-1992; U10166.
13-NOV-1991; US-791934.
(REGC ) UNIV CALIFORNIA.
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=
                                                                                                                                                              Mus musculus.
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(DOWC) DOW CHEM CO. (USSH) US DEPT HEALTH & HUMAN SERVICES. Gourlie BB, Kaplan DA, Mezes PS, Rixon MM, Schlom J;

16-FEB-1994; U01709. 16-FEB-1993; US-017570.

Anti-carcinoembryonic antigen chimeric light chain Ab. Anti-carcinoembryonic antigen chimeric antibodies; CEAS;

R60564 standard; Protein; 110 AA.

25-APR-1995 (first entry)

R60564:

chimeric human-murine; breast or colorectal carcinoma;

Chimeric Mus muscaris. Chimeric Homo sapiens.

WO9419466-A 01-SEP-1994

light chain.

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antibody against cancer-specific mucin. The coding sequence was isolated from Nd2 hybridoma cells expressing a murine antibody reactive with pancreatic cancer cells. The DNA encoding the antibody variable regions
                                                                                                                                                                                                                                                                                                                                                                          Claim 6; Page 16-17; 25pp; French.
The amino acid sequence of the variable region from the light chain of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     express a chimeric mouse-human antibody. The antibodies are useful in the detection and treatment of cancer. The chimeras should be less likely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                from the heavy (098533) and light chains were isolated and inserted into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  which additionally contain genes encoding the human constant domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 DIVLTQSPASLGVSLGQRATISCRASKSVSTSGYSYMHWYQQKPGQTPKLLIYLASNLES 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                     New variable domains of antibody recognising cancer specific mucin - and related DNA and expression vectors, producing chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 divltqspaslavslggratiscrasksvttsdfsymhwygqkpgppklllylasnles
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  These vectors express the domains as an Fv antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 725; DB 14; Length 112;
Pred. No. 1.52e-46;
                                                                                                                                                                                                                                                                                                                                                           mouse-human antibody for diagnosis and treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to cause anaphilaxis than the original murine antibody
                                                                                                                                                                                                                                                                   Chung Y, Iba Y, Kaneko T, Sowa M, Yasukawa K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 77.0%;
Local Similarity 91.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102; Conservative
                                                                                                                     by GAG*
93..101
                                                                  54..60
                                                                                                                                                                                                                               13-JAN-1994; JP-002131.
                                                                                                                                                                                                              3-JAN-1995; 000349.
                                                                                                      64
                                                                                                                                                                                                                                                 (TOYJ ) TOSOH CORP.
                                                                                                                                                                                                                                                                                  WPI; 95-247908/33.
                                                                                                        Misc difference
                                                                                                                        'note= "encoded
                                                                                                                                                                                                                                                                                                      N-PSDB; Q98534.
                                                                                                                                                                            FR2714915-A1.
                                                                                                                                                                                            .3-JUL-1995.
                                                    /label= CDR1
                                                                                      /label= CDR2
                                                                                                                                                         'label= CDR3
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vectors.
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1; 1 divltqspasltvslglratiscrasksvsasgysymhwyqqrpgqppklliylasnlqs 60 Gaps antigen during therapy. It can also be used in vivo diagnostically, or in therapy for the treatment of tumours associated with colorectal and breast carcinomas, as well those of the 21 DIVLIQSPASLGVSLGQRATISCRASKSVSTSGYSYMHWYQQKPGQTPKLLIYLASNLES Anti-carcinoembryonic antigen chimeric antibodies - for diagnosis Disclosure; Fig 2.2; 17pp; Japanese. Ab has binding specificity for P.aeruginosa exotoxin A without 4; Indels 1; N-terminal sequence of anti-pseudomonas aeruginosa exotoxin A and therapy of carcinoma, e.g. breast or colorectal carcinoma Anti-(pseudomonas aeruginosa) exotoxin a monoclonal antibody Query Match 76.0%; Score 716; DB 11; Length 110; Best Local Similarity 92.8%; Pred. No. 7.70e-46; Matches 103; Conservative 3; Mismatches 4; Indels Q71394 codes for R60564 the antibody light chain region of murine-human anti-carcinoembryonic antigen (CEA) chimeric antibody. Which can be used in in vitro immunoassays for the detection of CEA, and monitoring of tumour-associated ADP-ribotransferase; cytotoxin; enhancing factor 2; EF-2; for prevention, treatment and diagnosis of P. aeruginosa US-08-137-117B-25.rag Ì gastrointestinal tract, lung, ovary and pancreas. Location/Qualifiers Claim 11; Page 50; 67pp; English. R07456 standard; protein; 112 AA. 08-MAR-1989; 056666, 08-MAR-1989; JP-056666, (SUMO) SUMITOMO CHEM IND KK. (SUMI-) SUMITOMO SEIYAKU KK. 103; Conservative 04-FEB-1991 (first entry) 97..107 35..49 50..56 89..96 monoclonal Ab L-chain. 24..34 57..88 1..23 WPI; 90-325628/43. 110 AA; WPI; 94-294331/36 N-PSDB; Q71394 Ribosylation. Active-site /label=CDR2 Active-site /label≃CDR3 J02234695-A. Active-site Domain /label=FR2 17-SEP-1990 /label=CDR1 /label=FR3 /label=FR1 /label=FR4 infection Sequence Domain Domain Domain 61 숌 a ò ð

inhibiting ADP-ribosyltransferase activity in vitro, but inhibiting

US-08-137-117B-25 rag Tul 8 08:19

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in vivo ribosylation of protein synthesis enhancing factor The product is useful in treatment, diagnosis and research 888888

.aeruginosa associated diseases.

AA 23 is as yet undetermined 112 AA; Sequence

1; Gaps Score 706; DB 2; Length 112; Pred. No. 4.67e-45; 5; Indels 3; Mismatches Query Match 74.9%; Best Local Similarity 91.9%; Matches 102; Conservative

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염 δ

61 gvparfsgsgsgtdftlnihpveeedaatyycqhire-aytfgggtkleik 110

쇰 ð Search completed: Mon Jul 8 08:29:28 1996 Job time : 26 secs.

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n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn Mon Jul 8 08:38:26 1996; MasPar time 279.00 Seconds 1027.715 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-137-117B-26 (1-405) from US08137117B.seq 405 Title:

Description: Perfect Score: N.A. Sequence:

1 ATGGGATGGAGCGGATCTT.......CTCTGGTCACTGTCTCTGGA 405
TACCTACCTGGCCTAGAA......GAGACCAGTGACAGAGAGACT

TABLE default Scoring table:

Gap 6

Claim 135

264399 seqs, 353985056 bases x 2 Searched:

Dbase 0; Query 0

Nmatch STD

Minimum Match 0% Listing first 45 summaries Post-processing:

embl-new11 Database:

1:BCT 2:FUN 3:INV1 4:INV2 5:INV3 6:MAM 7:ORG 8:PLN 9:PR1 10:PR12 11:PR13 12:PR01 13:PR02 14:R0D 15:SYN 16:UNC 17:VRT 18:VIR

genbank 91 Database:

19:ECT 20:BCT2 21:BCT3 22:BCT4 23:BCT5 24:BCT6 25:BCT7 26:INV1 27:INV2 28:INV3 29:INV4 30:INV5 31:MAMI 32:MAM2 33:PAT1 34:PAT2 35:PAT3 36:PBC 37:PINJ 38:PINZ 39:PINZ 40:PIN4 41:PIN5 42:PAN6 43:PIN7 44:PRI1 45:PRI2 46:PRI3 47:PRI4 48:PRI5 49:PRI5 60:PRI7 51:PRI8 52:PRI9 53:ROD1 54:ROD2 55:ROD3 56:ROD4 57:ROD5 58:ROD5 56:ROD5 69:RD1 60:STR 61:STN 62:UNA 63:VRL1 64:VRL2 65:VRL3 66:VRL4 67:VRL5 68:VRL5 69:VRL5 71:VRL5

penbank-new11 Database:

72:BCT1 73:BCT2*74:INV1 75:INV2 76:MAM 77:PHG 78:PLN 79:PR11 80:PR12 81:PR13 82:ROD 83:STR 84:SYN 85:UNA

u-emb144 91

86:VRL 87:VRT

Database:

88:partl

Mean 10.395; Variance 4.346; scale 2.392 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

US-08-137-117B-26.rge Jul 8 08:32

SUMMARIES

	. °§	274	269	258	254	248	247	\sim	245	24	243	241	240	240	235	235	235	234	234	232	232	232	229	229	229	228	227	227	227	227	226	225	224	223	223	222	221	221	221	220	220	220	220	220	220	220
		076-			99e-	20e-	3e-	-9c	å	31e-	٨	4	4	39e-	å	<u>Б</u>	Jе-	8	-8e	9 6-	96-	-96 -	0e-	0e-	- 0	96	96	9	9e-	- 96	g	- 8	Jе-	و	န္	- 2e-	3e-	Э́е-	섫	å	ď	-e-	è-	f	4	Ze
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		1 8	TGH	851	MUSHA5	MUS I GHZ Z H	MUSHA3	MUSHA6	MUSIGHEV	MDIGMVAU	MUSHA4	A07953	MDIGMVBG	IGH	MUS I GHFX	105341	166	ANT	HSI	MUS I GGVB	E	IG4	MUSANTVDJ	A23165	MUSIGGVAZ	MUS I GHFY	MUSIGHADY	MMIG1KH3	MUSIHCB	MUS I GHXZ	MMIGIKH4	MMMAB1G3	MUS I GHVA	\$54755	E	MMIGHVDJ	N16	MMI GVH9	IGH	MMI GVHR1	MMU28805	MUSIGKXE	IGF.	MMU26990	MMZ 6990	MUSIGAZA
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		13	405	421	440	911	440	440	408	348	440	450	348	806	412	414	414	348	547	429	484	90	451	588	88	Ξ,	342	52	14	462	152	474	9	351	60	454	354	653	167	352	83	401	80	821	821	18
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	e	2	307	596	292	98	35	284	33	32	281	279	278	278	73	273	273	272	272	2	270	270	2	267	267	997	65	565	265	265	264	63	29	797	19	260	259	29	259	258	258	258	258	258	258	28
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ALI GNMENTS

Mouse IgMk rearranged heavy-chain mRNA variable region (V-D-J) anti-DNA_autoantibody. 15-MAR-1989 mRNA 462 bp MUSICKCLS DEFINITION RESULT

KEYWORDS

M20831

ACCESS ION

SOURCE

V-region; autoantibody; immunoglobulin heavy chain. Mouse (strain (NZBXW)F-1) spleen hybridoma cell line BXW-DNAl6, cDNA to mRNA.

Mus musculus ORGANISM

AUTHORS

TITLE

REFERENCE

88331394

MEDLINE

COMMENT

JOURNAL

sig_peptide

CDS

source

FEATURES

IIRNA

Location/Qualifiers δ Scheinberg, D.A. and Queen, C. /note="V-region" /note="putative" /codon_start=1 /codon_start=1 /codon start=1 /gene="IgH" 75.8%; 88.3%; /gene="IgH" Best Local Similarity 88.3%; Matches 354; Conservative partial, 61..405 1..405 NCBI gi: 195613 1..4051..60Mus musculus ۵ 92148135 antigen 101 sig peptide mat_peptide Query Match source ORGANISM BASE COUNT 121 DEFINITION 121 181 181 ACCESSION REFERENCE AUTHORS JOURNAL MEDLINE CDS KEYWORDS TITLE FEATURES COMMENT ORIGIN SOURCE В 셤 ð 셤 8 ð ð /codon_start=1 /translation="MGWSWIFLFLLSVTAGVHSEIQLQQSGAELVKPGASVKISCKAS GYSFTGYNMNWVKQSHGKSLEWIGNINPYYGSTSYNQKFKGKATLTVDKSSSTAYMQL NSLTSEDSAVYYCARKNYGSSFDYWGQGTTLTVSS" ö 1 (bases 1 to 462)
Kofler,R., Strohal,R., Balderas,R.S., Johnson,M.E., Noonan,D.J., Duchosal,M.A., Dixon,F.J. and Theofilopoulos,A.N.
Immunoglobulin kappa light chain variable region gene complex organization and immunoglobulin genes encoding anti-DNA Draft entry and computer-readable sequence [1] kindly submitted R.Kofler 28-JUL-1988. ggaaagagccttgagtggattggaaatattaatccttactatggtagtagtactagctacaat 291 241 CAGAAATTCAAGGGCAAGGCCACATTGACTGTGACAAATCTTCCAGCACACGCCTACATG 300 52 atgggatggagctggatctttctcttcttctgtcagtaactgcaggtgtccactctgag 111 172 tgcaaggcttctggttactcattcactggctacaacatgaactgggtgaagcagagcat 231 181 GGAAAGAGCCTTGAGTGGATTGGATATTTGATCCTTTCAATGGTGGTACTAGCTACAAC 240 292 cagaagttcaagggcaaggccacattgactgtagacaaatcttccagcacagcctacatg 351 1 ATGGGATGGAGGGGGATCTTTCTCTTCTCTCTGAGGAACTGCAGGTGTCTCACTCTGAG 60 /note="IgMk heavy chain precursor; NCBI gi: 196950' Gaps Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; ö Score 312; DB 56; Length 462; Pred. No. 4.07e-274; 0; Mismatches 19; Indels cageteaacageetgacatetgaggaetetgeagtetattaetgtgeaag 401 Eutheria; Rodentia; Myomorpha; Muridae; Murinae /note="Ig heavy chain signal peptide 113 t J. Clin. Invest. 82, 852-860 (1988) organism="Mus musculus" /note="Ig heavy chain" 108 g autoantibodies in lupus mice Location/Qualifiers 'note="IgMk mRNA" /codon_start=1 52..>462 /codon_start=1 115 c 1 Query Match 77.0%; Best Local Similarity 94.6%; Matches 331; Conservative 110..>462 52..109 ...>462 NCBI gi: 196949 ..462 Chromosome 12.

126 a

BASE COUNT

ORIGIN

232

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352 301

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RESULT

mat_peptide

US-08-137-117B-26.rge

/translation="MGMSMIFLELLSGTAĞVHSEVQLQQSGPELVKPGASVKISCKAS GYTFTDYNMHWVKQSHGKSLEMIGYIYPYNGGTGYNQKFKSKATLITVDNSSSTAYMDV ö Chimeric and humanized antibodies with specificity for the CD33 tgcaaggcttctggatacacattcactgactacaacatgcactgggtgaagcagagccat 180 240 GGAAAGAGCCTTGAGTGGATTGGATATTGATCCTTTCAATGGTGGTACTAGCTACAAC 240 MUSIGHM195 405 bp mRNA ROD 13-AUG-1992 Mus musculus Ig heavy chain mRNA V-region, from hybridoma M195 61 gtccagcttcagcagtcaggacctgagctggtgaaacctggggcctcagtgaagatatcc 120 9 9 Gaps Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; ggaaagagccttgagtggattggatatttatccttacaatggtggtactggctacaac 1 atgggatggagctggatctttcttcctctgtcaggaactgcaggcgtccactctgag 1 ATGGGATGGAGCGGGATCTTTCTTTCTCTTCTGTCAGGAACTGCAGGTGTCCACTCTGAG .; o /note="V-region; putative; NCBI gi: 195614" V-region; immunoglobulin; immunoglobulin heavy chain Co, M.S., Avdalovic, N.M., Caron, P.C., Avdalovic, M.V., Length 405; 0; Mismatches 47; Indels Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
1 (bases 1 to 405) 'product="immunoglobulin heavy chain" /product="immunoglobulin heavy chain" 106 c 105 g 93 t RSLTSEDSAVYYCARGRPAMDYWGQGTSVTVSS" Score 307; DB 56; Pred. No. 4.32e-269; Mus musculus hybridoma M195 cDNA to mRNA 'sequenced_mol="cDNA to mRNA" /tissue_type="hybridoma M195" /organism="Mus musculus" Immunol. 148, 1149-1154 (1992) /map="chromosome 12" /gene="IgH" /map="chromosome 12" /map="chromosome 12"

US-08-137-117B-26.rge

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S

/translation="MELDLSIPIURNCRCLSEVOLOGSCPELVKPCASVKMSCKASGY
TFTDYYMKWVKQSHGKSLEWIGDINPYNGGTSYNQKFKGKATLIVDKSSSTAYMQLAS
LTSEDSAVYYCARDSNYYFDYWGQGTTLIVSS"
113 c 104 g 104 t (bases 1 to 440)

Rueff-Juy, D., Marche, P.N., Drapier, A.-M. and Cazenave, P.-A.

Junctional diversity of H and L chains allows the coexpression of we mutually exclusive idiotopes (Idill04 and Idi558)

J. Immunol. 146, 4024-4030 (1991) ä aagttcaagggcaaggccacattgactgtagacaaatcctccagcacagcctacatg 300 Score 292; DB 55; Length 440; Pred. No. 4.99e-254; 0; Mismatches 42; Indels 4; Gaps 24-JUL-1991 /product="Ab 414.2 heavy chain variable and joining Mus musculus Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae. 1-region; V-region; immunoglobulin heavy chain. R00 MUSHAS 440 bp mRNA fouse active H-chain VJ region, 5' cds. /cell_line="hybridoma" /sequenced_mol="cDNA to mRNA" /organism="Mus musculus" /partial /note="NCBI gi: 193747" Location/Qualifiers 1..440 fus musculus cDNA to mRNA. /codon_start= 72.1%; Similarity 88.6%; 358; Conservative 4CBI gi: 193746 region

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US-08-137-117B-26.rgc

Db 1059 gtgcaagagggattacactggtttccttactgggccaaggactctggtcactgct 1118	RESULT 6 LOCUS MUSHA3 440 bp mRNA ROD 24-JUL-1991 DEFINITION Mouse active H-chain VJ region, 5' cds. ACCESSION M73330 KEYWORDS V-region; immunoglobulin heavy chain. SOURCE Mus musculus cDNA to mRNA. ORGANISM Mus musculus active to mRNA. Enkaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;	Eutheria; Rodentia; Myomorpha; Muridae; Murinae. REFERENCE 1 (bases I to 440) AUTHORS Rueff-Juy, D., Marche, P.N., Drapier, AM. and Cazenave, PA. TITLE Junctional diversity of H and L chains allows the coexpression of two mutually exclusive idiotopes (IdI104 and IdI558) JOURNAL J. Immunol. 146, 4024-4030 (1991) MEDLINE 91237115 COMMENT NCBI gi: 193742 FEATURES Location/Qualifiers source 1440	/organism="Mus musculus" /cell_line="hybridoma" /sequenced_mol="cDNA to mRNA" 39440 /partial /note="NCBI gi: 193743" /codon start=1 /product="Ab 262.9 heavy chain variable and joining region" /translation="MEIDLSIPIVRNCRCISEVQLQQSGPEIVKPGASVKASCKASCY	TFTDYTMGWRGSPGKSLEWIGDINPNNGGTSTNQKFKGRATLTVDKSSSTAYMQIAS LISEDSAVYCABORYWTFDVWGTGTVTVSS* BASE COUNT 114 a 114 c 110 g 102 t ORIGIN Query Match 70.4%; Score 285; DB 55; Length 440; Best Local Similarity 91.4%; Pred. No. 5.23e-247; Matches 320; Conservative 0; Mismatches 29; Indels 1; Gaps 1;	actgcagdtgtct-ctctgag 92 	0y 61 ATCCAGCTGCAGCTGCAGCTGAGCTGATGAAGCCTGGGGCTTCACTGAAGTTTC 120 Db 153 tgtaaggcttctggatacacattcactgactactacatgaagtggtgaagcagagccct 212	Db 213 ggaaagagccttgagtggattggagatattaatcctaacaatggtggtactagctacaac 272
Db 273 cagaagttcaagggcaaggccacattgactgtagacaaatcctccagcacagcctacatg 332	Db 393 tactactttgactactggggccaaggcacactctcacagtctc 436	germline; immunoglobulin heavy chain. us Animalia; Chordata; Vertebrata; Mammal Rodentia; Myomorpha; Muridae; Murinae. 1 to 2911) Taylor, L., Pollard, J.W. and Steele, E.J on of mutations around rearranged heavy	genes 10, 5187-5196 n/Qualifiers mm="Mus musculu ="C57BL/6J" ="C57BL/6J" cocies="domestic	BARE COUNT 828 a 557 c 675 g 851 t ORIGIN Query Match 70.6%; Score 286; DB 56; Length 2911; Best Local Similarity 91.2%; Pred. No. 5.20e-248; Matches 333; Conservative 0; Mismatches 29; Indels 3; Gaps 2; Db 759 caggigtcctctctgaggtccagctgcaacaatctggacctgagctggtgaagcctgggg 818	Qy 44 CAGGTGTCCACTGGGTGCAGCTGGAGGTTGGACCTGAGGTGAAGCCTGGGG 103 Db 819 cttcagtgaagatatcctgtaaggcttctggatacacgttcactgactactacatgaact 878	Db 879 gggtgaagcagtggaaagagccttgagtggattggagatattaatcctaacaatg 938	Oy 224 GTGGTACTAGCTACAACCAGAATTCAAGGGCAAGGCCACATTGACTGTGACAAATCTT 283 Db 999 ccagcacagcctacatggagctccgcagcctgacatctgaggactctgcagtctattact 1058

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Db 333 cagetcaacagoctgacatetgaggactctgcagtctattactgtgcaagagttacagt 392 	Db 393 tacgtctttgactactggggccaaggcaccactctcacagtctc 436 	RESULT 8 LOCUS MUSIGHFV 408 bp mRNA ROD 15-JUN-1988 DEFINITION Mouse Ig active alpha-chain V-JH1 region (J558 family) anti-dextran mRNA, hybridoma 45.21.1, subgroup 11. ACCESSION M12765 C-region; J-region; V-region; immunoglobulin heavy chain;	immunoqlobulin-alpha; processed gene; variable region subgroup II. Mouse (C57Bi,) hybridoma cell line 45.21.1, cDNA to Evkaryote; Animalia; Chordata; Vertebrata; Mammali; Eutheria; Rodentia; Myomorpha; Muridae; Murinae. E 1 (bases I to 408) Sikder, S.K., Akolkar, P.N., Kaladas, P.M., Morrison, S. Kabat, E.A.	TITLE Sequences of variable regions of hybridoma antibodies to alpha-(1->6) dextran in BALB/c and C57BL/6 mice JOURNAL J. Immunol. 135, 4215-4221 (1985) MEDLINE 86060914 COMMENT NCBI gi: 195309 FEATURES Location/Qualifiers Source /organism="Mus musculus" sig_peptide 1.57 sig_peptide 1.57		/note=1g H-chain V-JHl-region" /codon start=1 99 a 107 c 109 g 98 t	Query Match 69.9%; Score 283; DB 56; Length 408; Best Local Similarity 90.8%; Pred. No. 5.28e-245; Matches 315; Conservative 0; Mismatches 32; Indels 0; Gaps 0; Db 1 atgggatggagtggatcttctcttctctctgtcaggaactgcagtgtcctctcccga 60	Db 61 gtccagctgcaacagtctggacctgagctggtgaagcctcagtgaagatatcc 120
Qy 241 CAGAAATTCAAGGGCAAGGCCACATTGACTGTTGACAATCTTCCAGCACACCCTACATG 300 Db 333 cagctcaacagcctgacatctgaggactctgcagtctattactgtgcaag 382	301	RESULT 7 LOCUS MUSHA6 440 bp mRNA ROD 24-JUL-1991 LOCUS MUSHA6 H-chain VJ region, 5' cds. ACCESSION M14139 KEYWORDS J-region; V-region; immunoglobulin heavy chain. SOURCE Mus musculus cDNA to mRNA. ORGANISM Mus musculus cDNA to mRNA. Frikarvota: Animalia: Chordata: Vertebrata: Mammalia: Theria:	inae. inae. id Cazenave id Idi558)	ICG	/ LEGICAL MEIDLSILPINRNCRCISEVOLQOSCPELVKPGASVKMSCKASGY TETDYYMKWYKQSPCKSLEWICDINPNNGGTSYNQKFKGKATLITUDKSSSTAYMQLNS LTSEDSAYYCARDYSYPFDYWGQCTTLTVSS" LTSEDSAYYCARDYSYPFDYWGQCTTLTVSS" LTSEDSAYYCARDYSYPFDYWGQCTTLTVSS" COUNT 117 a 114 c 105 g 104 t ORIGIN Query Match 70.1%; Score 284; DB 55; Length 440;	75	93 gtccagctgcaacaatctggacctgagctggtaaagcctggggcttcagtgaagatgtcc 	 Qy 121 TGCAAGGCTTCTGGTTACTCATTCACTATACATACACTGGGTGAAGCAGCCGT 180 Db 213 ggaaagagcttgagttggatattaatcctaacaatggcggtactagctacaac 272

Ξ

Db 1 gaggtccagctgcagcagtctggacctgagctggtgaagcct.	61	Db 121 cctgaaaagagccttgagtggattggagattaatcctagc 	Db 181 aaccagaagttcaaggccacattgactgtagacaaa 	Db 241 atgragatctaagagcttgacatctgaggacttgcagtctat	SUL	MAGNICA CONTROL INTERPRETATION OF SECURITY	ORGANISM Mus musculus Eukaryota; Animalia; Chordata; Vertebrat Eutheria; Rodentia; Myomorpha; Muridae; REFERENCE I (bases I to 440)	AUTHORS Rueff-Juy, D., Marche, P.N., Drapier, AM. TITLE Junctional diversity of H and L chains a two mutually exclusive idiotopes (IdI104	JOURNAL J. Immunol. 146, 4024-4030 (1991) MEDLINE 91237115 COMMANT NCBI qi: 19374 FEATURES source Location/Qualifiers 1.440 CDS 39440 CDN CDN	/partial /note="NCBI gi: 193745" /codon_start=1 /product="Ab 16.3 heavy chain v regions" /translation="MELDLSLPLVRNCRCLS /translation="MELDLSLPLVRNCRCLS /TRTDYYMKWWGSPGKSLEWIGDISPNNGCT /ITSEDSAVYYCARDYDWYFDVMCTTVTVS //DYNGIN 114 a 112 c 110 g 104 t ORIGIN	y Match 69.4%; S Local Similarity 90.9%; P	Matches 318; Conservative U; Mismatches 31 Db 34 atgggatggagctggatctttctctctcttgtcaggaact
	241 cagaagttcaagggtaaggccacattgactgtagacaagtcctccagcacagcctacatg 300 	301 ggactccgcagcctgacatctgaggactctgcagtctattactgtgc 347 	9 MDIGMVAU 348 bp RNA ROD 01-APR-1993 M.domesticus IgM variable region.	Azzozo antibody; IgM gene; IgM variable region; immunoglobulin. western European house mouse. Mus musculus domesticus Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;	Sciurognathi; Myomorpha; Muridae; Murinae; Mus. 1 (bases 1 to 348) Tillman, D.M., Jou, N., Hill, R.J. and Marion, T.N. Both IgM and IgG anti-DNA antibody are the products of clonally	J. Exp. Med 1 (1922) In press 2 (bases 1 to 348) Marion, T.N.	Direct Submission Submitted (23-MAR-1993) to the EMBL/GenBank/DDBJ databases. Tony N. Marion, Microbiology and Immunology, University of, Tennessee, Membhis, 858 Madison Avenue, Memphis, TN, 38163, USA	NCBI gi:	/organism="Mus domesticus" /strain="(NZB x NZM)FI" /dev_stage="somatic variant" /tissue type="spleen" /cell_type="hybridoma" /cell_tine="17s.166" /isolate="mouse #17" /chromosome="12" /sex="Female"	<pre><1>348 /gene="NGBI gi: 288724" /note="NCBI gi: 288724" /note="NCBI gi: 288724" /codon start=1 /function="heavy chain variable region for IgM anti-DNA antibody; Vh558 family" /product="immunoglobulin variable region" /translation="EVQLQQSCPELVKPGXSVKISCKASCYSFTCYYMHWVKQSPEKS LEWIGEINPSTGGITYNQKFKAKATLTVDKSSSTAYWQLKSLTSEDSAVYYCARGRYT FAYWGOGTLUYPUSA</pre>	89 a 81 c 94 g 83 t	Query March 69.6%; Score 282; DB 35; Length 348; Best Local Similarity 90.2%; Pred. No. 5.31e-244; Matches 314; Conservative 1; Mismatches 33; Indels 0; Gaps 0;
l Qy 181 G		рь 301 g Qy 301 с	RESULT 9 LOCUS DEFINITION	REYNORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE	JOURNAL REFERENCE AUTHORS	TITLE JOURNAL	COMMENT FEATURES SOUICE		CDS	BASE COUNT ORIGIN	Query Match Best Local Matches 3

tactacatgcactggtgaagcaaagt 120 || || || || || || || || || || || || |IATTACATACACTGGGTGAAGCAGAGC 177

24-JUL-1991 ROD

lin heavy chain. 5' cds.

Vertebrata; Mammalia; Theria; Muridae; Murinae.

oler, A.-M. and Cazenave, P.-A.
c. chains allows the coexpression of
se (Idil04 and Idi558)

y chain variable and joining

IJVRNCRCLSEVOLQQSGPELVKPCASVKASCKASGY :DISPNNGGTSYNQKFKGKATLIVDKSSSTAYMQLNS :GTGTTVTVSS*

DB 55; Length 440; 5.33e-243; tches 31; Indels 1; Gaps

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10000	11 0 Vo. 32
10000	76 Off 0 In
1 100030	JULO UO: 32
1 100037	Jul 0 Vo.32

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Qy 121 TGCAAGGCTTCTGGTTACTCATTGACTATTACATACATGGGTGAAGCAGAGCAT 180	Db 219 ggaaggagccttgagtggattggatatattatccttacagtggtcctactggctacaac 278 	Db 279 cagagitcaacagcaaggcacattgactgtagacaattcctccagcacagcctcatg 338	Db 339 gaggtccgcagcctcgcagctctgcagtctattactgtgcagagagggatc 398	Db 399 ttctatact 407 Qy 361 CGCTTRGCT 369	RESULT 12 LOCUS MDIGMVBG 348 bp RNA ROD 05-NOV-1994 DEFINITION Widomesticus IgM variable region.	Σ	Eukaryotae; mitochondrial eukaryotee; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygli; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;	∺ %	117LE Both 1gH and 1gG antL-DNA antloodies are the products of cionally selective B cell stimulation in (NZB x NZW)FI mice intent I for Mod 176 (13) 751-770 (1002)		AUTHORS Marion, T.N. TITLE Direct Submission Indeed Submission Indeptate (72_mail 1023) to the FMBI //ConBank //NDBI databases from N	JOURNICO (127-20-1195) CO (THE ADDIVERSALING) CONTROL MATION, MISTODIOLOGY AND Immunology, University of, Tennessee, Memphis, 858 Madison Avenue, Memphis, TN, 38163, USA	COMMENT NCBI gi: 297745 FEATURES Location/Qualifiers Source /Arranism=Whis domestions	/detrain="(NZB x NZW)Fl" /dev stage="Somatic variant"	/LISSUE - Lype= spienn //cell_type="hybridoma" //cell_line="15.12" /isolate="mouse #25" //chromosome="12"	/sex="Female" CDS <1>348		/codon start=1 /function="heavy chain variable region for IgM anti-DNA antibody; Vh558 family"	<pre>/product="lnmunoglobulin variable region" /translation="QVQLQQSDRELVKPGXSVKISCKASGYTFTDYNMDWVKQSHGKS LEWIGYIYPNNGGTGYNQKFKSKATLTVDKSSSTAYMELHSLTSEDSAVYYCARGRYT</pre>
Qy 1 ATGGGATGGAGGGGGATCTTTCTCTTCCTTGTGAGAACTGCAGGTGTCCACTCTGAG 60	Db 93 gtccagctgcaacaatctggacctgagctggtaaagcctggggcttcagtgaagatgtcc 152 	Db 153 tgtaaggettetggatacacatteactgactactacatgaagtgggtgaagcagggecct 212 	Db 213 ggaaagagcttgagtggattggagatattagtcctaacaatggtggtactagctacaac 272 	Db 273 cagaagtcaagggcaaggcacattgactgtagacaaatcctccagcacagcctacatg 332 	Db 333 cagctcaacagccttacatctgaggactctgcagtctattactgtgcaag 382 	RESULT 11 LOCUS A07953 450 bp RNA PAT 01-SEP-1993 DEFINITION Artificial sequence for anti-hcG antibody.	ACCESSION A07953 KEYWORDS . SOURCE unidentified. ORGANISM unidentified	unclassilled. REFERENCE 1 (bases 1 to 450) AUTHORS van Wezenbeek, P.M.G.F. and Bos, E.S.	TITLE ARTI-DCG antibodies JOURNAL Patent: EP 0370581-A 9 30-MAY-1990;	COMMENT NCBI gi: 411512 FEATURES Location/Qualifiers	source 1450 /organism="Artificial sequences" cnc 20 Asto		/product="anti-hcG antibody" /translation="MGMSWHELFLEGGTAGWHSEVOLQQSGPELVKEGASVKISCKAS /translation="MGMSWHELFLEGGTAGWHSEVOLQQSGPELVWBGASVRISCKAS GTTDYNMHWYGSHGREEMICTITYPROPERTORYNGRENSKATLTVDNSSSTAFMEV BST-PSFDSAXYVARDECTEV*MMYVAGGGTGTAGWHSCS	BASE COUNT 116 a 116 c 113 g 105 t	Query Match 68.9%; Score 279; DB 33; Length 450; Best Local Similarity 87.8%; Pred. No. 5.37e-241; Matches 324; Conservative 0; Mismatches 45; Indels 0; Gaps 0;	Db 39 atgggatggatctttctcttctctctgtcaggaactgcaggcgtccactctgag 98	Qy 1 AIGGGAIGGAGCGGGAICTTICTCTTCTCTGGGAACTGCAGGTGTCCACTCTGAG 60	Db 99 gtccagcttcaacagtcaggacctgagctggtgaaacctggggcctcagtgaagatatcc 158	Db159 tgcaaggettettggatacacatteactgactacaacatgcactgggtgaagcagagccat218

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sig_peptide 14 source DEFINITION ORGANISM 1056 1116 936 401 **ACCESSION** REFERENCE AUTHORS MEDLINE REFERENCE AUTHORS JOURNAL JOURNAL SGS FEATURES KEYWORDS TITLE TITLE COMMENT RESULT SOURCE 임 유 a g 8 ð ð g ð 셤 à Š à Mouse Ig rearranged heavy chain gene V205.12-D-J region, hybridoma A20/44. ; ö Distribution of mutations around rearranged heavy-chain antibody 59 AGATCCAGCTGCAGCAGTCTGGACCTGAGCTGAAGCCTGGGGCTTCAGTGAAGATAT 118 62 cctgcaaggettctggatacacattcactgactacaacatggactgggtgaagcagagcc 121 122 atggaaagagccttgagtggattggatatttatcctaacaatggtggtactggctaca 181 accagaagttcaagagcaaaggccacattgactgtagacaagtcctccagcacagcctaca 241 61 tggagctccacagcctgacatctgaggactctgcagtctattactgtgcaagaggaggt 30) Gaps 25-JUL-1991 Gaps Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; 2 aggtccagctgcagcagtctgaccgtgagctggtgaagcctgggncttcagtgaagatat ñ ; 0 Length 2908; Length 348 1 others 2 others Indels 0; Mismatches 35; Indels Both, G.W., Taylor, L., Pollard, J.W. and Steele, E.J. 302 atacgtttgcttactggggccaagggactctggtcactgtctctgca 348 359 ACCGCTTTGCTTACTGGGGCCAAGGACTCTGGTCAGTCACTGTCTCTGCA 405 Muridae; Murinae 80 Score 278; DB 56; Pred. No. 5.39e-240; Pred. No. 5.39e-240; Score 278; DB 53; ų Mismatches V-region; immunoglobulin heavy chain. Mouse DNA. Mol. Cell. Biol. 10, 5187-5196 (1990) 90377208 820 /sub_species="domesticus" /sequenced_mol="DNA" 8 /organism="Mus musculus" /strain="C57BL/6J" Eutheria; Rodentia; Myomorpha; 6 9 L9 Location/Qualifiers 5 DNA 94 FAYWGQGTLVTVSA" 1 82 c 9 varialbe-region genes (bases 1 to 2908) 68.6**%**; 90.1**%**; 2908 bp Query Match 68.6%; Best Local Similarity 89.9%; 555 c Conservative 312; Conservative 1..2908 NCBI gi: 196346 Mus musculus Best Local Similarity Matches 329; Conser æ MUSIGHZZF 91 M58535 Query Match 13 source DEFINITION ORGANISM BASE COUNT Matches REFERENCE AUTHORS BASE COUNT 182 242 JOURNAL MEDLINE ACCESSION KEYWORDS TITLE FEATURES COMMENT ORIGIN SOURCE LOCUS

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756 caggtgtcctcttgaggtccagctgcaacaatctggacctgaacgggtgaagcctgggg 815

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MUSIGHFX 412 bp mRNA ROD 15-MAR-1990 Mouse Ig family J558 active mu-chain V-J3 region anti-dextran mRNA, Akolkar, P.N., Sikder, S.K., Bhattacharya, S.B., Liao, J., Gruezo, F., Morrison, S.L. and Kabat, E.A.
Errata: Different V-L and V-H germ-line genes are used to produce similar combining sites with specificity for alpha-(1->6) dextrans J. Immunol. 139, 3911-3911 (1987) Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

1 (bases 1 to 412)

Akolkar, P.N., Sikder, S.K., Bhattacharya, S.B., Liao, J., Gruezo, F., Morrison, S.L. and Kabat, E.A.

Different V-L and V-H germ-line genes are used to produce similar combining sites with specificity for alpha-(1->6) dextrans

J. Immunol. 138, 4472-4479 (1987) /note="Ig mu heavy chain V-J3-region; NCBI gi: 195314" 996 ccagcacagcctacatggagctccgcagcctgacatctgaggactctgcagtctattact 1055 935 995 343 224 GTGGTACTAGCTACAACCAGAAATTCAAGGGCAAGGCCACATTGACTGTTGACAAATCTT 283 peptide, 44 CAGGTGTCCACTCTGAGATCCAGCTGCAGAGTCTGGACCTGAGCTGATGAGACCTGGGG 876 gggtgaagcagagccatggaaagagccttgagtggattggagatattaatcctaacaatg 816 cttcagtgaagatttcctgtaaggcttctggatacacgttcactgactacatgaact C-region; J-region; V-region; immunoglobulin heavy chain; to mRNA /note="Ig mu heavy chain V-J3-region signal immunoglobulin mu-chain; processed gene. Mouse (BALB/c) hybridoma cell line 9.14.7., cDNA /organism="Mus musculus" <1...55 Location/Qualifiers /codon_start=2 <1..>412 /codon start=2 (bases 1 to 56) hybridoma 9.14.7. [2] revises [1] NCBI gi: 195313 Mus musculus 87224123 ctgca 1120 CTGCA 405

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YTFTDYYMKAWYRQSHGKSLEWIGDINPNNGGTSYNQKEKGKATLTVDKSSSTAYMQLN SLTSEDSAVYYCARDYYGSSSFVYMGQGTLVTVSV" translation="WSWIFLEXLLSGTAGVLSEVQLQQSGPELVKPGASVKISCKASG"

/note="Ig mu heavy chain V-J3-region" 56..>412 mat_peptide

3 others 105 /codon start=1 9<u>4</u> c 105

105 g Chromosome 12. æ BASE COUNT

ORIGIN

Length 412; Score 273; DB 56; L Pred. No. 5.47e-235; y Match 67.4%; Local Similarity 91.1%; hes 317; Conservative Query Match

2; 1 atgaagctggatctttctcttcnnnctcttgtcaggaactgcaggtgtcctctctgaggt 60 Gaps 3 Indels 0; Mismatches 28; Matches 쇰

6 ATGGAGCGGGATCTTTCTCTTCT--TCT-GTCAGGAACTGCAGGTGTCCACTCTGAGAT 62 ð

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14-NOV-1994 15 RESULT

PAT 0256654 Sequence 3 from patent EP 105341 414 bp Unknown. Unknown 105341 DEFINITION ORGANISM ACCESSION KEYWORDS SOURCE

Chimeric rodent/human immunoqlobulin specific for tumour-associated Patent: EP 0256654-A2 3 24-FEB-1988 antigens JOURNAL

1 (bases 1 to 414) Schoemaker, H.J. and Sun, L.K.

Unclassified

REFERENCE AUTHORS

TITLE

Location/Qualifiers /organism="unknown" 1..414 NCBI gi: 591098 source FEATURES COMMENT

Score 273; DB 35; Length 414; Pred. No. 5.47e-235; 106 115 g th 67.4%; Similarity 83.7%; 339; Conservative Ų 97 æ 96 Query Match Best Local S COUNT ORIGIN BASE

10 atggaatggagcagagtctttatcttctcctatcagtaactgcaggtgttcactcccag 용

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99

Mismatches

Matches

189 180 300 369 120 181 GGAAAGAGCCTTGAGTGGATTGGATATTGATCCTTTCAATGGTGGTACTAGCTACAAC 240 250 gagaagttcaagggcaaggcaacactgactgcagacaaatcctccagcactgcctacatg 309 8 tgcaaggcttctggatacgccttcactaattacttgatagagtgggtaaagcagaggcct 70 gtccagttgcagcagtctggagctgagctggtaaggcctgggacttcagtgaaggtgtcc cagctcagcagcctgacatctgatgactctgcggtctatttctgtgcaagagtggtccc 1 ATGGGATGGAGCGGGATCTTTCTCTTCTTCTGTCAGGAACTGCAGGTGTCACTCTGAG 130 190 310 301 ζ 유 g δ g δ 임 g ð ð ð

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

Mon Jul 8 08:43:30 1996; MasPar time 35.45 Seconds 759.603 Million cell updates/sec Run on:

n.a. - n.a. database search, using Smith-Waterman algorithm

MPsrch_nn

Tabular output not generated.

>US-08-137-117B-26 (1-405) from USO8137117B.seq 405 Title:

Description: Perfect Score: N.A. Sequence:

1 ATGGGATGGAGCGGATCTT......CTCTGGTCACTGTCTCTGGA 405
TACCTACCTACCTCGCCCTAGAA......GAGACGAGTGACAGAGAGGTGT

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 Nmatch STD

84802 seqs, 33246950 bases x 2 Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

n-geneseq22 Database:

i.parti 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16

Mean 8.356; Variance 5.470; scale 1.528 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	1.82e-238	2.77e-172	4.11e-167			-		5.56e-151	2.45e - 150
Description	p12-h2.	KM-750 heavy chain.	KM-796 heavy chain.	Sequence encoding hea	Sequence encoding mou	Heavy chain variable	DREG-200 Ab heavy cha	Co-1 Heavy Chain V Re	Encodes murine monocl
ID	030754	Q45428	045426	012058	012014	004695	00/990	008607	011291
DB	5	11	11	7	7		11		7
\$ Query Match Length DB	405	443	449	474	474	450	420	471	499
% Query Match	99.5	74.3	72.3	69.1	69.1	68.8	66.4	66.2	62.9
Score	403	301	293	280	280	279	569	268	267
Result No.	П	7	m	4	ß	9	7	∞	6

	2.45e-150	7	.25e-1	4	.25e-14	4	2.97e-143	4.89e-140	.16e-1	3.52e-136	.52e-1		1.55e-135	1,55e-135	1,55e-135	2.98e-134	1.11e-131	1.11e-131	4.85e-131	4.08e-129	1.79e-128	1.79e-128	7.84e-128	7.84e-128	7.84e-128	3.43e-127	1.50e-126	1.50e-126	1.50e-126	6.58e-126	2.88e-125	2.88e-125	1.26e-124	1.26e-124	5.51e-124
US-08-137-117B-26.mg	H-chain V-region of m	-	Plasmid pAH4808.		Plasmid pAH4807.	Sequence encoding hea	Monoclonal antibody M	DNA sequence of the V	CTMO1 VH cDNA.	MAb SCH94.03 heavy ch	Sequence encoding mou	Sequence encoding hea	U7.6 heavy chain vari	p64-h2.	Sequence encoding mur	81C6 heavy chain vari	PB1.3 heavy chain sig	Hypercalcaemia agent	2H7 Vh sequence.	Fv(GP-4) immunosuppre	Sequence of the anti-	Sequence of the anti-	Heavy chain variable	Mouse C4G1 Ig heavy-c	VH186 region of anti-	Genomic sequence enco	Mouse anti-HIV mu5.5	Anti HIV antibody hea	pLCB7 insert.	2H7 VH sequence which	Heavy chain variable	Monoclonal antibody 0			Sequence of VHinge ge
US-08-137	043385	043846	043848	043844	043847	006955	048037	N91820	038877	T05312	Q12013	012057	069933	030758	045593	073405	051549	028522	N91146	673679	N70968	L960LN	097498	045663	015164	006957	065553	070371	030904	N70971	097501	012637	066846	9	Q20380
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	588	10704	10844	11529	12132	444	1581	443	416	429	477	477	360	417	453	099	342	326	458	729	420	420	348	414	458	2675	354	354	461	459	344	1570	408	411	474
	65.9		64.9	64.9	64.9	64.2	63.2	62.0	61.2	60.5	60.5	60.5	60.2	60.2	60.2	59.8	58.8	58.8	58.5	57.8	51.5	57.5		57.3	57.3	57.0	56.8	56.8	56.8	9	56.3	9	9	56.0	55.8
33	267	263	263	263	263	260	256	251	248	245	245	245	244	244	244	242	238	238	237	234	233	233	232	232	232	231	230	230	230	229	228	228	227	227	226
Jul 8 08:33	10	12	13	14	15	16	11	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

																			_	-	\	
				light chain; L; H;	hybridoma; AUK12-20;												,	7	a M;	7		-e receptor -
	Q30754 standard; cDNA; 405 BP.	first entrv)		<pre>Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;</pre>	neavy chain; variable region; mouse; monoclonal; hybridoma; AUK12-20;	plasmid; p12-k2; p12-h2; ss.		Location/Qualifiers	157		58405				.00544.	P_09547.6.	P-032084.	SEIYAKU KK.	Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;	:/48.	_	Reconstituted human antibody to human interleukin-6 receptor
111	030754 standar	30-MAR-1993 (first entry)	p12-h2.	Human; antibod	heavy chain; v	plasmid; p12-k	Synthetic.	Key	sig_peptide	/*tag= a	mat peptide	/*tag= b	W09219759-A.	12-NOV-1992.	24-APR-1992; J00544.	25-APR-1991; JP-095476.	19-FEB-1992; JP-032084.	(CHUS) CHUGAI SEIYAKU KK.	Bendig MM, Jon	WPI; 92-398882/48.	P-PSDB; R28669.	Reconstituted
RESULT	25	i i	吕	Ž	Ž	₹	os	표	F.	H	Ţ	F	M	PD	뫈	PR	PR	PA	ΡΙ	DR	DR.	PT

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Sequence 405 BP; 97 A; 97 C; 106 G; 105 T; Gaps Disclosure; Page 119-120; 207pp; Japanese. The sequences given in Q30753-54 were used in example to illustrate the production of a human antibody which recognises human interleukin-6 receptor (IL-6R). The antibody comprises light (L) antigenicity and contains mouse V-region complementarity ö Monoclonal antibody; Ab; ganglioside GMZ; chimera; chimera; chimeric antibody; Ab; ganglioside GMZ; chimeric antibody; expression vector; heavy; light; chain; hypervariable region; CDR; constant region; hybridoma; Iq; immunoglobulin; KM-796; KM-750; KM-603; cancer; ss. Mus musculus.

Location/Qualifiers
CDS
33.,443 1; Indels Query Match 99.5%; Score 403; DB 5; Length 405; Best Local Similarity 99.8%; Pred. No. 1.82e-238; 361 cgctttgcttactggggccaagggactctggtcactgtctctgca 405 0; Mismatches /note= "hypervariable region 1" Q45428 standard; cDNA; 443 BP ng stop codon" 33..89 17-NOV-1994 (first entry) determining regions
Disclosure; Page 119-120; 404; Conservative /note= "sig_peptide" KM-750 heavy chain. /*tag= a /note= "excluding misc feature sig_peptide /*tag= b 301 Matches 181

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er.	9
Υ E	/note= "hypervariable region 2" misc feature 384.410
	0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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- 0	17-WAR-1994. 07-SEP-1993; 046181.
- E	JP-238452. HAKKO KOGYO KK.
H I	Hanai N, Hasegawa M, Koike M, Kuwana Y, Nakamura K;
Sign	Shitara K; 11. 94-12657/16. D-Denn: D53330
. .	y specific for
<u>ā</u> , č	producing a cytocidal effect on cancers such as melanoma,
Ä	Disclosure, Page 107-108; 191pp; English.
ਹ∓	nimeric human Ab expression vectors are constructed by inserting ne Ab heavy and light chain variable region-encoding cDNA
-≓	isolated from hybridomas producing a mouse or rat monoclonal Ab
ĭš	eacting with the ganglioside GMZ respectively into an expression ector for use in animal cells which contains the human Ab heavy and
-	ight chain constant region-encoding cDNA. The expression vectors
ਲ -ਜੋ	re introduced into animal ceils and the transformant thus obtained s cultured for the prodn. of a chimeric human Ab reacting with the
Ď.	anglioside GM2. In contrast to mouse monoclonal Abs, the chimeric
ă, ā	uman Abs Will not cause anti-mouse ig Ab prodn. In the patient s ody but show a prolonged blood half-life, with a reduced frequency
0 +	f adverse effects, so that it can be expected to be superior
0 0 2	concert for instance.
ÈĚ	chain sequences are given in Q4542
<u></u>	CDR regions for use in chimeric Abs are indicated in the
Š	Sequence 443 BP; 109 A; 112 C; 119 G; 103 T;
uer est atc	Query Match 74.3%; Score 301; DB 11; Length 443; Best Local Similarity 90.3%; Pred. No. 2.77e-172; Matches 371; Conservative 0; Mismatches 34; Indels 6; Gaps
	33 atgggatggatctttctcttcttcttctggaggactgcaggtgtctctctgag 92
	1 ATGGGATGGAGGGGGATCTTTCTCTTCTTCTTCTTCTGGAACTGCAGGTGTCCACTCTGAG 60
	93 gtccagctgcagcagtctggacctgagctggtgaagcctggggcttcagtgaagatatcc 152
	61 ATCCAGCTGCAGCAGTCTGCACCTGAGCTGTGAGCCTGGGGCTTCAGTGAGATATCC 120
	153 tgcaaggettetggatacacatteactgactacaacatggactgggtgaagcagagecat 212
	121 TGCAAGGCTTCTGGTTACTCATTCACTAGCTATTACATACA
	2]3 ggaaagagcottgagtggattggatatattatootaacaatggtggtaotggotacaac 272
	181 GGAAAGAGCCTTGAGTGGATTGGATATTGATCCTTTCAATGGTGGTACTAGCTACAAC 240
	273 cagaagttcaagagcaaggccacattgactgtagacaagtcctccagcacagcctacatg 332
	241 CAGAAATTCAAGGGCAAGGCCACATTGACTGTGACAAATCTTCCAGCACACGCTACATG 300
	333 gagetecacageetgaeatetgaggaetetgeagtetattaetgtgeaagageggggagg 392

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3 neuroblastoma and glioma.
Claim 5; Page 104-105; 191pp; English.
Chimeric human Ab expression vectors are constructed by inserting the Ab heavy and light chain variable region-encoding CDNA isolated from hybridomas producing a mouse or rat monoclonal Ab reacting with the ganglioside GM2 respectively into an expression vector for use in animal cells which contains the human Ab heavy and ganglioside GM2. In contrast to mouse monoclonal Abs, the chimeric human Abs will not cause anti-mouse Ig Ab prodn. in the patient's body but show a prolonged blood half-life, with a reduced frequency of adverse effects, so that it can be expected to be superior to mouse monoclonal Abs in the efficacy in the treatment of human are introduced into animal cells and the transformant thus obtained is cultured for the prodn. of a chimeric human Ab reacting with the light chain constant region-encoding cDNA. The expression vectors Monoclonal antibody; Ab; ganglioside CM2; chimera; chimeric antibody; expression vector; heavy; light; chain; hypervariable region; CDR; constant region; hybridoma; Ig; immunoglobulin; KM-796; KM-750; KM-603; cancer; ss. Humanised antibody specific for ganglioside GM2 - used for producing a cytocidal effect on cancers such as melanoma, Koike M, Kuwana Y, Nakamura K; Location/Qualifiers /*tag= c /note= "hypervariable region 1; /*tag= e /note= "hypervariable region 3; /*tag= d /note= "hypervariable region 2; .T 3 Q45426 standard; cDNA; 449 BP. /note= "excluding stop codon" sig_peptide 33..89 (KYOW) KYOWA HAKKO KOGYO KK. Hanai N, Hasegawa M, Koike //tag= b /note="sig_peptide" /note="sig_peptide" 17-NOV-1994 (first entry) 237..287 384..416 33..449 07-SEP-1992; JP-238452. cancer, for instance. 07-SEP-1993; 046181. KM-796 heavy chain. WPI; 94-126857/16. P-PSDB; R53328. misc_feature misc_feature Mus musculus AU9346181-A. 17-MAR-1994 Shitara K; /*tag= a claim 8" claim 8" claim 8" 045426;

DAC DAC DAC DATE OF THE PROPERTY OF THE PROPER

Sequence Query Match

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112 gtccagctgcaacagtctggacctgaactggtgaagcctgggggcttcagtgaagatatcc 171 caqaaqttcaaqqacaaqqccacattqattqtaqacaaqtcctccaqcacaqcctacatq 351 301 CATCTCAGCAGCCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGGGGGGGTAAC 360 352 gacgtccgcagcctgacatctgatgattctgcagtctattactgtgcaagaagagaaat tgcaagacttctggatacacattcactgaatacaccatacactgggtgaagcagagccat abortion; tumour detection; complementary determining regions; produced by a bacterial, yeast or mammalian expression system. Sequence 474 BP; 123 A; 118 C; 112 G; 121 T; murine variable regions. These novel sequence are useful in treatment, diagnosis and prophylaxis of HIV infections, and /product=hCG-binding protein heavy chain variable region misc feature 187..200 0; Mismatches 42; Indels Query Match 69.1%; Score 280; DB 2; Lk Best Local Similarity 88.5%; Pred. No. 1.02e-158; Matches 322; Conservative 0; Mismatches 42; Location/Qualifiers ₩. 04-OCT-1990 (first entry) Q04695 standard; DNA; 450 390..416 247..293 pregnancyprevention; ss. 39..449 1..6 /label=EcoRI-linker ctct 415 CGCT 364 Mus musculus. misc feature misc_feature /product=CDR misc feature /product=CDR misc feature /product=CDR Φ /*tag= c Q 004695; /*tag= /*tag= /*tag= 172 25 232 181 292 241 412 361 Key RESULT g ð 888888 g ð 염 g ð 염 ð g ð g δ ð ö 112 gtccagctgcaacagtctggacctgaactggtgaagcctggggcttcagtgaagatatcc 171 61 ATCCAGCTGCAGCTCTGGACCTGAGCTGAAGGCTGGGGCTTCAGTGAGATATCC 120 231 291 181 GGAAAGAGCCTTGAGTGGATTGGATATATTGATCCTTTCAATGGTGGTACTAGCTACAAC 240 cagaagttcaaggacaaggccacattgattgtagacaagtcctccagcacagcctacatg 351 352 gacgtccgcagcctgacatctgatgattctgcagtctattactgtgcaagaagaggaat 411 1 ATGGGATGGAGGGGATCTTTCTCTTCTTCTGTCAGGAACTGCAGGTGTCCACTCTGAG 60 Gaps diagnosis ggacagagcettgagtggattggaggtattaateetaacaatggtggtactaectacaac 172 tgcaagacttctggatacacattcactgaatacaccatacactgggtgaagcagagccat 2G12 since they have an increased compatibility in humans. The heavy and light chain V-regions are joined by manipulating their respective joining (J) regions, to generate restriction enzyme recognition sites. The chimeric MAbs can be used as immuno-The mouse VH gene product may be used to produce chimeric mouseconjugates, in association with e.g. toxins for HIV treatment. They can also be used in diagnosis of HIV. See also Q12056-57 and Q12059-63. ; 121 T; Score 280; DB 2; Length 474; Pred. No. 1.02e-158; 0; Mismatches 42; Indels in treatment, RR; Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson WPL; 91-178106/24. P-PSDB; R12234. chain V region 112 G; nsed 118 C; 1 New chimeric mouse human antibodies and prophylaxis of HIV infections. Disclosure; Fig 7; 108pp; English. Sequence encoding mouse MAb 2G12 H HIV-1; chimera; ds. Location/Qualifiers 52..474 Q12014 standard; DNA; 474 BP 123 A; 69.1**%**; 88.5**%**; 19-AUG-1991 (first entry) 322; Conservative 13-NOV-1990; U06627. 13-NOV-1989; US-433703. Best_Local Similarity Matches 322; Conserv 474 BP; (XOMA-) Xoma Corp.

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ይ regions and against HIV-1 comprising human Ig constant

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Length 474;

Gaps ; 0

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11 atgggatggagctggatctttctcttctcctgtcaggaactgcaggtgtcctctctgag

9 1 ATGGGATGGAGCGGGATCTTTCTTTCTTTCTTGTCAGGAACTGCAGGTGTCCACTCTGAG 61 ATCCAGCTGCAGCACTTGAGCTGATGAAGCCTGGGGCTTCAGTGAAGATATCC 120

231

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411 Heavy chain variable domain of human chorion gonadotrophin-binding pptd. Human chorionic gonadotropin; antibodies; heavy chain; choriocarcinoma;

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Mus sp.

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pregnancy, for combatting choriocarcinomas or other hCG-producing tumours
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                                                                                                                                                                                                                                                                                                                               to a constant region of human origin. The product can be used to prevent
                                                                                                                                                                                                                                                                                                                                                                       They also have diagnostic applications as immune reagents for in vivo diagnosis, eg for localisation of tumours and for in vitro diagnosis for
                                                                                                                                                                                                                                                                                                          (FhCG). For the production of antibodies the variable region was fused
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ggaaggagccttgagttggattggatatatttatccttacagtggtcctactggctacaac 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 gtccagcttcaacagtcaggacctgagctggtgaaacctggggcctcagtgaagatatcc 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AICCAGCTGCAGCAGTCTGGACCTGAGCTGATGAAGCCTGGGGCTTCAGTGAAGATATCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159 tgcaaggcttctggatacacattcactgactacaacatgcactgggtgaagcagagccat 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 IGCAAGGCTICTGGTTACTCATTCACTAGCTATTACATACACTGGGTGAAGCAGAGCCAT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cagaggttcaacagcaaggccacattgactgtagacaattcctccagcacagccttcatg 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 CAGAAATTCAAGGGCAAGGCCAACATGACTGTGACAAATCTTCCAGGACAGCCTACATG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gaggtccgcagcctgacatctgaagactctgcagtctattactgtgcaagagagggatc 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 CATCTCAGCAGCCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGGGGGGGTAAC 360
                                                                                                                                                                                                                                                              myeloma cell line. Togheter with the heavy chain variable domain (Q04694) the sequence forms a hCH-binding antibody encoding fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atgggatggagctggatctttctcttcctctgtcaggaactgcaggcgtccactctgag 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATGGGATGGAGCGGGATCTTTCTCTTCTCTGTCAGGAACTGCAGGTGTCCACTCTGAG 60
                                                                                                                                                            Polypeptide(s) which specifically bind human chorionic gonadotropin contg. antigen-binding domains comprising complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DREG-200 Ab heavy chain variable region.
DREG-200; L-selectin; LECAM-1; Mel-14; LAM-1; humanized antibody; immunoglobulin; Ig; IgG1; IgG4; complementarity determining region; CDR; monoclonal antibody; MAb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                     determining domains.
Disclosure; p; English.
The variable fragment was isolated from an anti-hCG-producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 279; DB 1; Le
Pred. No. 4.49e-158;
                                                                                                                                                                                                                                                                                                                                                                                                                                   116 C; 113 G;
                                                                                                                                                                                                                                                                                                                                                                                                                  detection of hCG in body fluids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q66700 standard; cDNA; 420 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                     116 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 68.9%;
Best Local Similarity 87.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-NOV-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324; Conservative
                                                         25-NOV-1988; NL-002902.
                                        21-NOV-1989; 202951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ttctatact 407
                                                                                                                  WPI; 90-165307/22.
P-PSDB; R05090.
                                                                                                   van Wezenbeek PM;
                                                                                (ALKU) AKZO NV.
EP-370581-A. 30-MAY-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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121 tgcaaggcttctggatacacattcactagctatgttatgcactgggtgaagcagaagcct 180 gagaagttcaaaggcaaggccacactgacttcagacaaatcctccagcacagcctacatg 300 61 gtccagctgcagcagtctggacctgacctggtaaagcctggggcttcagtgaagatgtcc 120 61 ATCCAGCTGCAGCAGTCTGGACCTGAGCTGAAGCCTGGGGCTTCAGTGAAGATATCC 120 241 CAGAAATTCAAGGCCAAAGGCCACATTGACTGTTGACAAATCTTCCAGCACAGCCTACATG 300 1 atggaatggagttggatatttctctttctcctgtcaggaactgcaggtgtccactctgag 60 9 chain variable region frameworks of the human acceptor antibody Eu. Nucleotide and as sequences are provided for the DREG-200 light (Q66699, R55553) and heavy (Q66700, R55554) chain variable regions and the humanized DREG-200 light (Q66701, R55555) and heavy (Q66702, R55556) chain variable regions. The humanized antibodies can be produced economically in large quantities by expression in mammalian 0; Gaps gggcagggccttgagtggattggatatatttatccttacaatgatggtactaagtacaat Eu; transgenic animal; ss. to Ba Disclosure, Fig. 1B; 60pp; English. An L-selectin-specific IgG1 or IgG4 humanized antibody has CDRs corresponding to those of mouse MAb DREG-200 and heavy and light 301 gagctcagcagcttgacctctgaggactctgcggtctattactgtgcaagggagg 355 New humanised antibody specific for L-selectin - with murine (and human framework regions, inhibits binding of neutrophils tendothelial cells and useful for treating or preventing 66.4%; Score 269; DB 11; Length 420; 87.9%; Pred. No. 1.26e-151; 0; Mismatches 43; Indels 106 T; framework; light chain; heavy chain; variable domain; monoclonal antibody; acceptor antibody Eu; transgenic 115 G; cell culture or in transgenic animals. Sequence 420 BP; 101 A; 98 C; Location/Qualifiers 1..57 (PROT-) PROTEIN DESIGN LABS INC. 312; Conservative US-983946. Best Local Similarity 09-JUN-1994. 30-NOV-1993; Ull612. WPI; 94-199974/24. P-PSDB; R55554. inflammation /*tag= a mat_peptide 01-DEC-1992; W09412215-A. sig_peptide Query Match Mus sp. Co MS; Matches 181 241 181 g 엄 g 음 음 g ð ð δ õ ð δ

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JLT 8 Q08607 standard; DNA; 471

RESULT ID O

008607;

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දු 셤 g g ð 유 δ ò ð ö chimeric antibody mol. comprising two light chains and two heavy chains, each having a constant region (human) and a variable region (murine) 52 atggaatggagttggatatttctctttctcctgtcaggaactgcaggtgtccactctgag 111 gtccagctgcagcagtctggacctgagctggtaaagcctggggcttcagtgaagatgtcc 171 61 ATCCAGCTGCAGCAGCTTGAGCTGATGAAGCCTGGGGGCTTCAGTGAAGATATCC 120 172 tgcaaggcttctggatacacatttactagctatgttatgcactgggtgaagcagaagcct 231 351 300 they are more compatible with the human body. They are esp. used for gggcagggccttgagttggattggatatattaatccttacaatgatggtactagttacaat 291 (MAD) Co-1. The chimeric antibodies can be used for any purpose for which the original murine MADs can be used, with the advantage that having specificity to an antigen bound by murine monoclonal antibody 0; Gaps Claim 13; Page 123 + Fig 22; 173pp; English. Shown is the nucleotide sequence from the end of the oligo-dC tail to the Jh4-Ch1 junction. The sequence is used in the prodn. of a 241 CAGAAATTCAAGGCCAAGGCCACATTGACTGTTGACAAATCTTCCAGCACAGCCTACATG gagcccttcaaaggcaaaggccacactgacttcagacaaatcctccagcacagcctacatg Chimeric mouse-human antibodies - prepd. using genes coding for constant human region murine variable region, esp. to 3 tumour Co-1 Heavy Chain V Region (mouse).
Monoclonal antibody; chimera; light; heavy; chain; constant; variable; antigen; diagnosis; cancer; tumour; ss. Score 268; DB 5; Length 471; Pred. No. 5.56e-151; 121 T; 0; Mismatches 43; Indels Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP; WPI; 90-115825/15. 115 G; 120 C; the diagnosis and treatment of cancer. Location/Qualifiers 115 A; (ITGE-) INT GENETIC ENG INC Query Match 66.2%; Best Local Similarity 87.9%; (first entry) 311; Conservative 06-SEP-1989; U03852. 06-SEP-1988; US-241644. 13-SEP-1988; US-247744. 13-SEP-1988; US-247739. 19-UN-1989; US-267641. 21-JUL-1989; US-382768 P-PSDB; R09425 musculus W09002569-A 22-MAR-1990 Sequence Query Match antigen /*tag= 232 292 Matches 112 181 352 Mus NAME OF THE PROPERTY OF THE PR g q ò 음 ð 용 음 g ð ð ð ð

cagaagttcaagggcaggggcacattgactgtagacaaatcgtccagcacagcctacatg 340 library was enriched for full-length L- and H-chains. It was screened 41 atgggatggacctggatctttattttaatcctgtcggtaactacaggtgtccactctgag 100 101 gtccaactgctgcagtctggacctgagctggagaagcctagcgcttcagtgatgatatcc 160 61 ATCCAGCTGCAGCTGTGGACCTGAGCTGATGAAGCCTGGGGGCTTCAGTGAAGATATCC 120 161 tgcaaggettetggtteeteatteaetggetacaacatgaaetgggtgaggeagaaeatt 220 181 GGAAAGAGCCTTGAGTGGATTGGATATTGATCCTTTCAATGGTGGTACTAGCTACAAC 240 esp. antibodies, by transfecting host cell with constructed cassette and second DNA sequence Example; Fig 2; 52pp; English.

Two separate H and L chain CDNA libraries were prepared from mRNA isolated from the murine hybridoma cell line 14.18. The lambda gt10 Gaps encode a normal length Ig leader peptide. To ensure translation starts from the second ATG codon once additional 5' sequences have analysis. The longest H cDNA sequence was sequenced. It appears to 1 ATGGGATGGAGCGGGATCTTTCTTTTCTCTTCTGGAACTGCAGGTGTCCACTCTGAG chimaeric binding protein; immunoglobulin; variable region; mouse; æ 221 ggaaagagccttgaatggattggagctattgatccttactatggtggaactagctacaac been added to the insert, the cDNA is truncated by limited Bal31 exonuclease treatment. An XhoI linker was then added to give a sequence which, when expressed, will result in an mRNA encoding a by filter hybridisation using various C region probes. Ten phage clones from each screening were analysed further by restriction **:** Fusion protein prodn. - e.g. having dual biological activity, Ig leader sequence and a functional variable region. 122 T; Query Match 65.9%; Score 267; DB 2; Length 499; Best Local Similarity 87.8%; Pred. No. 2.45e-150; Matches 310; Conservative 0; Mismatches 43; Indels 119 G; Encodes murine monoclonal 14.18 H chain V region 131 C; Location/Qualifiers ₩. 127 A; (ABBO) ABBOTT LABORATORIES. Q11291 standard; cDNA; 499 14-JUN-1991 (first entry) 98..499 20-SEP-1989; US-409889. 41..97 01-AUG-1990; U04301 499 BP; WPI; 91-117518/16. P-PSDB; R11597. See also 011292 Mus musculus. /*tāg= a sig_peptide 04-APR-1991. WO9104329-A. mat peptide Gillies SD: Sequence /label= 011291; normal 281 Key

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QQ	434 gagctccgcagcctgacatctgaggacactgcagtctattactgtgcaagaggggattc 493
δy	301 CATCICAGCAGCCTGACGACTCTGGAGGTCTTATTACTGTGCAGGGGGGGTAAC 360
Ωp	ccctatg
δy	361 CGCTTTG 367
- 52	11
	Q43843 standard; DNA; 417 BP.
	043043; 20-OCT-1993 (first entry)
	Chimeric 128.1 VH, mouse gamma subgroup IIB DNA.
3	Polymerase chain reaction; primer; PCR; amplify; murine; heavy;
5 5	receptor; antibody; brain; capillary; endothelial cell; conjugate;
X	neuropharmaceutical; diagnostic; agent; tumour; AIDS; stroke;
X 8	epilepsy; Farkinsons disease; Alzhelmers disease; ss. Sunthatic
SE	
H	sig peptide 157
I II	/"tag= a /note= "Leader sequence"
F	mat_peptide 58417
E N	/*tag= b W09310819_A
E 62	10-JUN-1993,
PF	24-NOV-1992; U10206.
PR 8	26-NOV-1991; US-8UU458.
PI	Friden PM:
DR.	WPI; 93-196742/24.
E E	7
E. F	Antibody conjugates specific for transferrin receptor - used for
7 E	diagnosis and treatment of cancer, Aids and heurological disorders
PS	Table 6; Page 57; 151pp; English.
8	The sequences given in 043842-43 encode the light and heavy chains,
3 5	respectively, of the Chimeric antibody 128.1. 128.1 is an anti-numan
3 8	on brain capillary endothelial cells. This antibody may be used in a
8	conjugate in which it is linked to a neuropharmaceutical or diagnostic
ខ	agent. The conjugate may be used to treat or prevent neurological
8 8	disorders eg. brain tumours, AlDS, stroke, epilepsy, Parkinsons and Alzhaimers disease. It may also be used for diagnostic methods.
og S	Sequence 417 BP; 108 A; 104 C; 102 G; 103 T;
õ	Omery Match 64.9%: Score 263; DB 7; Length 417;
i di E	Similarity 87.3%; Pred. No. 9.25e-14 08; Conservative 0; Mismatches 4
q	1 atggaatggagctgggtaatgctcttcctcctgtcaggaactgcaggtgtccgctctgag 60
ē	
Ž	01.00001.00000000000000000000000000000
g	61 gtccagctgcaacagtctggacctgaactggtgaagcctggagcttcaatgaagatttcc 120
δ	61 ATCCAGCTGCAGCAGTCTGGACTGATGAGCCTGGGGCTTCAGTGAAGATATCC 120
원	121 tgcaaggcttctggttactcattcactggctacaccatgaactgggtgaagcagagccat 180

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Plasmid pAH4808. Synthetic. methods. Query Match /*tag= /note= " 043848; /*tag= unsure 1968 2028 Кеу 888888888888888888 셤 염 අ g 음 염 8 ID DE DE DE DE CONTROL à à à à ð heavy; light; chain; variable; constant; region; anti-human; pAH4807; transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2; endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4; 241 cagaagttcaaggacaaggcccctttaactgtagacaagtcatccaacacagcctacatg 300 Disclosure; Fig 17A-F; 151pp; English.
The sequences given in Q4346-48 represent the expression vectors pAH4625, pAH4807 and pAH4808. These vectors represent the cloning of the different human gamma isotypes, gamma-2, gamma-3 and gamma-4 respectively, with the variable region of the minne monoclonal antibody 128.1. These plasmids each encode a chimeric monoclonal 181 ggagagaaccttgagtggattggacgtattaatcctcacaatggtggtactgactacaac Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625 antibody in which the heavy chain (VH) is derived from a murine 301 gagctcctcagtctgacatctgaggactctgcagtctattactgtgcaagagg 353 301 CATCTCAGCAGCCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGGGG 353 diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal; Parkinsons disease; Alzheimers disease; SP2/0 cell; ss. Antibody conjugates specific for transferrin receptor - used for diagnosis and treatment of cancer, AIDS and neurological /*tag= a /note= "Sequence not given in the specification" rns 1848..2552 /note= "Sequence not given in the specification" "Sequence not given in the specification" 4318..4517 "Chimeric 128.1 VH/CH1 region" Location/Qualifiers Q43846 standard; DNA; 10704 BP. 20-0CT-1993 (first entry) 3099..3425 4012..4311 11..1710 "Undefined ORF1" 26-NOV-1991; US-800458. "Undefined ORF2" (ALKE-) ALKERMES INC. 24-NOV-1992; U10206. WPI; 93-196742/24. P-PSDB; R41707-09. Plasmid pAH4625 W09310819-A 10-JUN-1993 Synthetic. Friden PM; v ø disorders

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ö appropriate bands for the heavy and light chains as well as the assembled antibody for the gamma-3 and gamma-4 chimeras. No detectable receptor on brain ceceptor antibody which binds to the transferrin receptor on brain capillary endothelial cells. This antibody may be used in a conjugate in which it is linked to a neuropharmaceutical or diagnostic agent. The conjugate may be used to treat or prevent neurological disorders eg. brain tumours, AIDS, stroke, epilepsy, Parkinsons and Alzheimers disease. It may also be used for diagnostic 2027 2087 2088 cagaagttcaaggacaaggccctttaactgtagacaagtcatccaacacagcctacatg 2147 protein was isolated for the gamma-2 transfectants. 128.1 is an anti-1908 gtccagctgcaacagtctggacctgaactggtgaagcctggagcttcaatgaagatttcc 1967 source and the sequences encoding CH1, CH2 and CH3 are derived from a human source. These vectors in combination with the chimeric light chain vector, pAG4611 (see also Q43845), were transfected into SP2/0 cells and clones were isolated. Antibody analysis using biosynthetically labelled proteins, immunoprecipitation and SDS-PAGE indicated 1848 atggaatggagctgggtaatgctcttcctcctgtcaggaactgcaggtgtccgctctgag 1907 61 AFCCAGCTGCAGCTCTGGACCTGAGCTGATGAAGCCTGGGGCTTCAGTGAAGATATCC 120 300 heavy; light; chain; variable; constant; region; anti-human; pAH4807; 9 transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2; endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4; ggagagaaccttgagtggattggacgtattaatcctcacaatggtggtactgactacaac 241 CAGAAATTCAAGGGCAAGGCCACATTGACTGTTGACAAATCTTCCAGCACAGCCTACATG tgcaaggettetggttactcattcactggctacaccatgaactgggtgaagcagagccat 181 GGAAAGAGCCTTGAGTGGATTGGATATATTGATCCTTTCAATGGTGGTACTAGCTACAAC Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; 2031 T; 2148 gagctcctcagtctgacatctgaggactctgcagtctattactgtgcaagagg 2200 diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal; ; 0 64.9%; Score 263; DB 7; Length 10704; Best Local Similarity 87.3%; Pred. No. 9.25e-148; Matches 308; Conservative 0; Mismatches 45; Indels Parkinsons disease; Alzheimers disease; SP2/0 cell; ss. 2130 G; 2189 C; "Murine 128.1 VH/human gamma-4 CH1" Location/Qualifiers 2070..3769 2125 A; LT 13 Q43848 standard; DNA; 10844 BP 3907..4611 20-OCT-1993 (first entry) Sequence 10704 BP;

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Location/Qualifiers
                                                                                                                                                                                                              Q43844 standard; DNA; 11529 BP
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/note= "Leader sequence"
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"Undefined ORF2"
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26-NOV-1991; US-800458.
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Parkinsons and Alzheimers disease. It may also be used for diagnostic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein was isolated for the gamma-2 transfectants. 128.1 is an anti-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chain vector, pAC4611 (see also Q43845), were transfected into SP2/0 cells and clones were isolated. Antibody analysis using biosynthetically labelled proteins, immunoprecipitation and SDS-PAGE indicated appropriate bands for the heavy and light chains as well as the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source and the sequences encoding CH1, CH2 and CH3 are derived from a human source. These vectors in combination with the chimeric light
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human transferrin receptor antibody which binds to the transferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibody 128.1. These plasmids each encode a chimeric monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnostic agent. The conjugate may be used to treat or prevent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibody in which the heavy chain (VH) is derived from a murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                  respectively, with the variable region of the murine monoclonal
                                                                                                                                                                                                                                                                                                                              Antibody conjugates specific for transferrin receptor - used for diagnosis and treatment of cancer, AIDS and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.9%; Score 263; DB 7; Length 10844;
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                             5153..5482
                                                              /note= "Undefined ORF2"
CDS 5580..5900
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c "Undefined ORF1"
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"Undefined ORF3"
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WPI; 93-196742/24.
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4147 cagaagttcaaggacaaggcccctttaactgtagacaagtcatccaacacagcctacatg 4206 4087 ggagagaaccttgagtggattggacgtattaatcctcacaatggtggtactgactacaac 4146 181 GGAAAGAGCCTTGAGTGGATTGGATATTTGATCCTTTCAATGGTGGTACTAGCTACAAC 240 Antibody conjugates specific for transferrin receptor — used for diagnosis and treatment of cancer, AIDS and neurological This vector contains open reading frames encoding the heavy heavy; light; chain; variable; constant; region; anti-human; Polymerase chain reaction; primer; PCR; amplify; murine; This sequence represents the expression vector pAH4602. US-08-137-117B-26.mg transferrin; receptor; antibody; brain; capillary; endothelial cell; conjugate; neuropharmaceutical; diagnostic; agent; tumour; AIDS; stroke; epilepsy; Parkinsons disease; Alzheimers disease; ss. Disclosure; Fig 11A-G; 151pp; English. /note= "VH and CH DNA derived by PCR" Jul 8 08:33

US-08-137-117B-26.mg

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625;
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                                     selection marker. Transcription of the VH gene is from the VH promoter of the murine 27.44 gene. The vector also includes a heavy chain immunoglobulin enhancer and the human
                                                                                                                                 plasmid pAH4274. This was achieved by digesting the plasmid and the product with EcoRV and NheI. The VH gene was inserted in-frame with the human gammal CH region CH at the 3' end of the VH-J region by means of a NheI site. 128.1 is
                                                                                                                                                                                                                                                                                                                                                                                                  Score 263; DB 7; Length 11529;
Pred. No. 9.25e-148;
                                                                                                                                                                                                                                                   cells. This antibody may be used in a conjugate in which it
                                                                                                                                                                                                                                                                                                                              Parkinsons and Alzheimers disease. It may also be used for
                                                                                                                                                                                                       an anti-human transferrin receptor antibody which binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 45; Indels
                                                                                              gammal constant region (CH). The VH region of 128.1 was isolated by polymerase chain reaction and cloned into
                                                                                                                                                                                                                                                                     is linked to a neuropharmaceutical or diagnostic agent.
                     ampicillin resistance gene and a histidine (histidinol)
                                                                                                                                                                                                                                the transferrin receptor on brain capillary endothelial
                                                                                                                                                                                                                                                                                           conjugate may be used to treat or prevent neurological
                                                                                                                                                                                                                                                                                                                                                                    2148 G;
                                                                                                                                                                                                                                                                                                              disorders eg. brain tumours, AIDS, stroke, epilepsy,
   chain variable region (VH) of the antibody 128.1,
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Best Local Similarity 87.3%;
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                                                                                                                                                                                                                                                                                                                                                    diagnostic methods.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      assembled antibody for the gamma-3 and gamma-4 chimeras. No detectable protein was isolated for the gamma-2 transfectants. 128.1 is an anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a human source. These vectors in combination with the chimeric light chain vector, pAG4611 (see also Q43845), were transfected into SP2/0 cells and clones were isolated. Antibody analysis using biosynthetically labelled proteins, immunoprecipitation and SDS-PAGE indicated appropriate bands for the heavy and light chains as well as the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               used in a conjugate in which it is linked to a neuropharmaceutical or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ይ
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The sequences given in Q43846-48 represent the expression vectors pAH4625, pAH4807 and pAH4808. These vectors represent the cloning of the different human gamma isotypes, gamma-7, gamma-3 and gamma-4 respectively, with the variable region of the murine monoclonal antibody in which the heavy chain (VH) is derived from a murine source and the sequences encoding CH1, CH2 and CH3 are derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor on brain capillary endothelial cells. This antibody may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neurological disorders eg. brain tumours, AIDS, stroke, epilepsy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnostic agent. The conjugate may be used to treat or prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 64.9%; Score 263; DB 7; Length 12132; Best Local Similarity 87.3%; Pred. No. 9.25e-148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibody conjugates specific for transferrin receptor - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for diagnosis and treatment of cancer, AIDS and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2285 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2441 C;
                                                               /note= "128.1 VH/human gamma-3 CH1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2292 A;
                                                                                                                                                                                                                                                                                                                                                                                                        4099..4419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4630..5559
1848..2546
                                                                                                                                                                                            3133..3177
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                                                                                                  2939..2980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Undefined ORF4"
                                                                                                                                                                  "Undefined ORF1"
                                                                                                                                                                                                                                                                                                                                                                        /note= "Undefined ORF3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-NOV-1991; US-800458.
                                                                                                                                                                                                                                                                  /note= "Undefined ORF2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12132 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ALKE-) ALKERMES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-NOV-1992; U10206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; R41710-14.
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WO9310819-A.
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q	1908	1908 gtccagctgcaacagtctggacctgaactggtgaagcctggagcttcaatgaagatttcc 196/	191
Qy	61	61 ATCCAGCTGCAGCACTCTGACCTGATGAAGCCTGGGGCTTCAGTGAAGATATCC 120	02
qq	1968	tgcaaggettetggttactcattcactggctacaccatgaactgggtgaagcag	2027
δλ	121	TGCAAGGCTTCTGGTTACTCATTCACTATTACATACACTGGGTGAAGCAGAGCCAT	180
QQ Q	2028		187
δλ	181		01
QQ	2088		147
δ	241	CAGABATTCAAGGGCAAGGCCACATTGACTTTGACAAATCTTCCAGCACGCCTACATG 300	00
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à	301		

Search completed: Mon Jul 8 08:44:12 1996 Job time : 42 secs.

Jul 8 08:33

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n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch nn Mon Jul 8 08:44:30 1996; MasPar time 187.70 Seconds 775.696 Million cell updates/sec Run on:

Tabular output not generated.

Title:

>US-08-137-117B-26 (1-405) from USO8137117B.seq 405 Description:

1 ATGGGATGGAGCGGGATCTT.....CTCTGGTCACTGTCTCTGCA 405 TACCCTACCTCGCCCTAGAA......GAGACCAGTGACAGAGACGT Perfect Score: N.A. Sequence: Comp: Scoring table:

TABLE default Gap 6

Dbase 0; Query 0 STD Nmatch 518261 seqs, 179750453 bases x 2 Searched:

Listing first 45 summaries Minimum Match 0% Post-processing:

Database:

1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8 9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14 15:EST15 14:EST14 15:EST15 14:EST14 15:EST15 14:EST14 15:EST15 14:EST14 15:EST15 14:EST16 17:EST27 23:EST27 24:EST27 25:EST27 25:EST27 25:EST27 25:EST27 25:EST27 25:EST27 25:EST27 25:EST28 23:EST33 34:EST33 34:EST34 35:EST33 34:EST33 34:EST33 34:EST33 34:EST33 34:EST34 35:EST35 35:EST35 35:EST35 35:EST35 35:EST35 35:EST35 35:EST36 25:EST46 45:EST46 45:EST47 48:EST49 45:EST55 56:EST66 65:EST66 67:EST67 68:EST66 65:EST66 67:EST67 68:EST68 69:EST67 77:EST77 77:EST77 73:EST73 74:EST74 75:EST75 75:EST75 75:EST75 75:EST76 77:EST77 77:EST77 73:EST73 74:EST74 75:EST76 75:EST76 77:EST77 73:EST73 74:EST74 75:EST76 75:EST76 77:EST76 77:EST77 73:EST73 74:EST74 75:EST75 75:EST76 77:EST76 77:EST76 77:EST77 73:EST73 74:EST74 75:EST76 77:EST76 77:EST77 73:EST73 74:EST74 75:EST76 77:EST77 73:EST73 74:EST76 77:EST76 77:EST77 73:EST73 74:EST76 77:EST77 73:EST73 74:EST76 77:EST76 77:EST77 73:EST73 74:EST76 77:EST77 75:EST77 77:EST77 77:

Database:

95;qnEST1 96;qnEST2 97;qnEST3 98;qnEST4 99;qnEST5 100;qnEST6 101;qnEST7 102;qnEST8 103;qnEST9 104;qnEST10 105;qnEST1 106;qnEST1 107;qnST22 108;qnST31 109;qnEST1 111;enEST1 111;enEST2 111;enEST3 112;enEST4 113;enEST5 114;enEST1 112;enEST1 112;enEST1 112;enEST1 112;enEST1 112;enEST1 125;enEST1 125;enEST1 125;enEST1 125;enEST1 125;enEST1 126;enEST1 126;

US-08-137-117B-26 rat Jul 8 08:37 128:enEST20 129:enEST21 130:enSTS1 131:enSTS2 132:enSTS3

Mean 10.062; Variance 1.818; scale 5.534 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Pred. No.	1.46e-157	1.46e-157	9.24e-1	24e-14	9.47e-	7e-1	. 76e-	.35e-6	1.35e-	76e-56	9.76e	53e-4	.53e-40	,53e-4	536	1.08e	<u>-</u> 3	3.11e-	3.11e-33	3.58e-	58e-2	.50e-1	3.50e-		3.50e-	.50e-1	.32e-1	.68e-1	68e-13	.68e-1	4.68e-	m	. 68e-	. 68e-1	<u>-</u>	54e-1	4.67e-10	4.67e-10	4.67e-10	4.67e-10	4.67e-10	4.67e-10	4.67e-10	4.67e-10	4.67e-10
Description	EST101034 Homo sapien	101034 Ношо	гв9669 ношо	9669 Ното в	Г61186 Ното	Ношо в	2	Ношо в	EST13874 Homo	scrofa mRNA; e	mRNA;	Homo s	1 Ното в	rl Homo		EST18962 Homo sapiens	Homo sapi	rl Homo	:1 Homo sa	1 Homo	rl Homo s	Ното	1 Homo	1 Нопо в	Ното в	ошо ва	rl Homo	j68a01.rl Homo	ST73046 Homo s	Homo	EST30734 Homo sapiens	ОШО	EST91759 Homo sapiens	Homo sa	yc01g07.rl Homo sapie	1 Homo	EST89449 Homo sapiens	EST89449 Homo sapiens	rl Homo	.rl Homo	3.rl Homo	rl Homo s	rl Homo s	566f01.rl Ношо в	yo66f01.rl Homo
ID	T27609	127	S 67	967	33	•	ã	7727	127	1010	SSCID10	T64512	R83139	ب	\sim	HST2		m	37	375	in		HS771238	_	HST27715	T27715	H24604	R48619		_	HST28164	_	HS71611	T29716	T60021	H22104	T29661	HS 66110	H27953	H44273	HS273234	T93178	R71741	H45128	HS128238
0.8	69	127		70	125		28	69	127		129	79	57		124	127				123	16	~		16	127	69	Ξ	47	0	_	127	9	122	20	78	10	70	122	12	11	117	87	53	11	114
Length	287	. 287	238	238	209	209	382	299	299	330	330	169	303	419	419	297	297	430	430	478	478	16	16	147	331	331	228	169	174	174	234	234	325	325	367	369	253	253	309	362	362	434	446	471	471
* Query Match	24.7	24.7	23.5	23.5	21.7	, i	17.8	13.3	13.3	12.6	12,6	10.6	10.6	10.6	10.6	10.4	•			8.6		-	7.2		7.2		•		6.7		•	٠	•	6.7	6.4	6.4		6.2	6.2		6.2	•		6.2	
Score	100	120	95	92	88	88	72	24	24						43	42	45	39	39	32	32	29	53	29	53	53	58	27	27	27	27	23	27	27	56	56	25	25	25	52	25	52	52	52	25
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ALI GNMENTS

EST HRNA đ 287 T27609 RESULT LOCUS

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ACCESSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

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US-08-137-117B-26 rat

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NOTITION AND A STATE OF THE STA		Qy 121 TGCAAGGCTTCTGGTTACTCATTCACT	121 TGCAAGGCTTCTGGTTACTCATTACATTACATACATGGGTGAAGAGAGGCCAT 180
ACCESSION KEYWORDS SOURCE	16.7009 EST. EST. Shiman primor=M13 Reviered library=Human Danrread	Db 194 ggacaagggcttgaatggatgggat	ggacaagggcttgaatggatgggtggatgaacctcgcagtggtgccacaaact 248
ORGANISM	Home sapiens	Qy 181 GGAAAGACCTTGAGTGGATTGGAT	181 GGAAAGAGCCTTGAGTGGATTGGATATTGATCCTTTCAATGGTGGTACTAGCT 235
	Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;	SULT 2	
REFERENCE	Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 287)		287 BP.
AUTHORS	Adams, m.D., Netlavage, m.K., Freischmann, K.D., Fuidher, K.A., Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,		ated, Version 3)
	White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,MW., Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,		EST101034 Homo sapiens cDNA 5' end similar to immunoglobulin mu heavy chain, VDJC regions (GB:M18512) (HT:3056).
	FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M.,		
	Globek, A., Glemm. C.L., Manna, M.C., Reublom, E., Minkle Jr, K.S., Kelley, J.M., Klimek, K.M., Kelley, J.C., Liu, LI., Marmaros, S.M.,		nomo sapiens (numan) Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
	Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pellegring, S.M., Philling, C.A., Ryder, S.E., Scott, J.T.	OC Theria; Eutheria; Primates; Ha	Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
	Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R.,	RP 1-287	
	Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,EJ., Dimke,D., Feng,P., Ferrie,A.,	RA Adams M.D., Kerlavage A.R., Fl. RA Bult C.J., Lee N., Kirkness E.	eischmann R.D., Fuldner R.A., F., Weinstock K.G., Gocavne J.D.,
	Fischer, C., Hastings, G.A., He, WW., Hu, JS., Greene, J.M.,	RA White O., Sutton G., Blake J.A	", Brandon R.C., Chiu M.W.,
	Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,YF., Wing,J., Xu,C.,	RA Clayton R.A., Cline R.T., Cott. RA FitzGerald L.M., FitzHugh W.M.	on M.D., Earle-Hughes J., Fine L.D., , Fritchman J.L., Geoghagen N.S.M.,
	Yu, GL., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A.,	RA Glodek A., Gnehm C.L., Hanna M	.C., Hedblom E., Hinkle Jr P.S.,
TITLE	Haseltine,W.A., Fleids,C., Fraser,C.M. and Venter,J.C. Initial Assessment of Human Gene Diversity and Expression Patterns	RA Kelley J.M., Klimek K.M., Kello RA Merrick J.M.; MORENO-PALANOUES	ey J.C., Liu L.I., Marmaros S.M., R.F., McDonald L.A., Nquyen D.T.,
Temanor	Based Upon 52 Million Basepairs of cDNA Sequence	RA Pellegrino S.M., Phillips C.A.	, Ryder S.E., Scott J.L.,
COMMENT	Unpublished (1995)	RA Saudek D.M., Shirley R., Small RA Weldman J.F., Li Y., Bednarik	A Saudek D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R., A Weidman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A.,
	Contact: Venter, JC The Institute for Canomic Research	RA Coleman T.A., Collins E.J., Dis	mke D., Feng P., Ferrie A.,
	932 Clopper Rd, Gaithersburg, MD 20878	RA Gruber J., Hudson P., Kim A.,	Kozak D.L., Kunsch C., Ji H., Li H.,
	Tel: 3018699056 Fax: 3018699423	RA Meissner P.S., Olsen H., Raymo, RA Yu G.L., Ruben S.M., Dillon P.	Meissner P.S., Olsen H., Raymond L., Wei Y.E., Wing J., Xu C., Yu G.L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A.,
	Email: tdbinfo@tdb.tigr.org		ser C.M., Venter J.C.;
	For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tabinfoatch tier ord).	RT "Initial Assessment of Human Gene Diversity and Expression RT Fatterns Based Upon 52 Million Basepairs of cDNA Sequence"; R. Innuhlished	ene Diversity and Expression Basepairs of cDNA Sequence";
	י לאדיי		ute for Genomic Research 932 Clopper
FEATURES	NCB1 g1:		kd, Gartherspurg, MD 20878 Tel: 3018699955 Fax: 3018699423 Email: tdbinfo@tdb.tigr.org For clone availability, additional sequence
sonrce	e 128/ /organism="Homo sapiens"		ated to this EST, please contact the r.org). NCBI qi: 609707
r NOW	/note="human"		fiers
BASE COUNT	62 a	source	
OKIGIN		:	o saptens"
Query Match Best Local Matches 1	tch al Similarity 71.1%; Score 100; DB 69; Length 287; 167: Conservative 0; Mismatches 68: Indels 0; Gaps 0;	FT mRNA <1>287 SQ Sequence 287 BP; 62 A; 77 C; 85 G; 60 T; 3 other;	5 G; 60 T; 3 other;
Db 14 a	gacctggaggatcctctttggtggcagcanaggagcccactccaq 73	Query Match 24.7%; Sc Best Local Similarity 71.1%; Pr	Score 100; DB 127; Length 287; Pred. No. 1.46e-157;
Qy 1.7		datches	0; Mismatches 68; Indels 0; Gaps 0;
Db 74 c	gtgcacctggtgcagtctggggtgaagatgaagacttggggcctcagtgaaggtctcc 133	14	alggactggactggaggatcctcttcttggtggcagcagccaacccaaccccag 73
Qy 61 P	61 ATCCACTGCACACTTGCACCTCATCAACCTCGCCCTTCAGTCAATCC 120		TOUTICIGICAGGAACIGCAGGIGICCACICIGAG BU
Db 134 t	134 tgcaagacttctggatacgccttcaccgactactatatacactggattcgacaggcccct 193	Db 74 gtgcacctggtgcagtctggggctg 	74 gtgcacctggtgcagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcc 133

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Adams N.D., Netlavage A.R., Figiscimania N.D., Fudater K.A.,

Bult C.J., Lee N., Kirkess E.F., Weinstock K.G., Gocayne J.D.,

Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D.,

Electrald L.M., FittHugh W.M., Fritchman J.L., Geoghagen N.S.M.,

Glodek A., Gohm C.L., Hanna M.C., Hedblom E., Hinkle Jr P.S.,

Relley J.M., Klimek K.M., Kelley J.C., Liu L.I., Marmaros S.M.,

Merrick J.M., MORENO-PALANQUES R.F., McDonald L.A., Nuyen D.T.,

Relley J.M., Shirley R., Small K.V., Spriggs T.A., Uterback T.R.,

Relley D.M., Shirley R., Small K.V., Spriggs T.A., Uterback T.R.,

Reldem J.A., Li Y., Bednarik D.P., Cao L., Cepeda M.A.,

Rischer C., Hastings G.A., He W.W., Hu J.S., Greene J.M.,

Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li H.,

Meisner P.S., Olsen H., Raymond L., Wei Y.F., Wing J., Xu C.,

N. Welley W.A., Fields C., Fraser C.M., Venter J.C.;

Initial Assessment of Human Gene Diversity and Expression

The Pattern Based Upon 52 Million Basepairs of CDNA Sequence*; tgcaagacttctggatacgccttcaccgactactatacactggattcgacaggcccct 193 Gaps and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org). NCBI gi: 611768 Contact: Venter, JC The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878 Tel: 3018699056 Fax: 3018699423 Email: 08-SEP-1995 (Rel. 45, Last updated, Version 2) ESTR9669 Homo sapiens cDNA 5' end similar to immunoglobulin heavy tdbinfo@tdb.tigr.org For clone availability, additional sequence 194 ggacaagggcttgaatggatgggatggatgaaccctcgcagtggtgccacaaact 248 ö Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae. Score 95; DB 122; Length 238; Pred. No. 9.24e-147; 1-238
Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A.,
Adams M.D., Kerlavage A.R., Fleischmann R.D., Gocayne J 0; Mismatches 51; Indels Sequence 238 BP; 46 A; 70 C; 69 G; 52 T; 1 other; /organism="Homo sapiens' standard; RNA; EST; 238 BP. chain V region (GB:X61012) (HT:3230). Location/Qualifiers 09-JAN-1995 (Rel. 42, Created) 08-SEP-1995 (Rel. 45, Last upd /note="human" 23.5**%**; 74.0**%**; 145; Conservative Homo sapiens (human) Best Local Similarity Unpublished Query Match LT 3 HS67011 source Matches 134

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Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M., Glodek, A., Gnehm, F.L., Hanna, M.C., Hedblom, E., Hinkle Jr, P.S., Kelley, J.M., Klimek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L.,
Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R.,
Weidman, J.F., Li, Y., Bedharik, D.P., Cao, L., Cepeda, M.A.,
Coleman, T.C., Collins, E.—J., Dim, P.D., Feng, P., Ferrie, A.,
Fischer, C., Haatings, G.A., He, W.—W., Hu, J.—S., Greene, J.M.,
Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Initial Assessment of Human Gene Diversity and Expression Patterns For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; EST89669 Homo sapiens cDNA 5' end similar to immunoglobulin heavy Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., 103 gitcagciggigcagictggagcigaggigaagaagcciggggccicagigaaggictcc 162 61 ATCCAGCTGCAGCTGTGGACCTGAGCTGAGCCTGGGGCTTCAGTGAAGATATCC 120 163 tgcaaggettetggttacacetttaccagetacggtateagetgggtgegacaggeeet 222 06-SEP-1995 Eutheria; Archonta; Primates; Catarrhin; Hominidae; Homo human primer=M13 Reverse library=Human Small intestine Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C. Based Upon 52 Million Basepairs of cDNA Sequence EST The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878 Tel: 3018699056 chain V region (GB:X61012) (HT:3230). /organism="Homo sapiens" /note="human" IRNA Location/Qualifiers Email: tdbinfo@tdb.tigr.org (tdbinfo@tdb.tigr.org) 238 bp Contact: Venter, JC (bases 1 to 238) 223 ggacaagggcttgagt 238 Unpublished (1995) <1..>238 Fax: 3018699423 NCBI gi: 611768 Homo sapiens T29670 T29670 4 source DEFINITION

source

6 69 U 2 46 BASE COUNT ORIGIN

1 others

52 t

Gaps : Score 95; DB 70; Length 238; 0; Mismatches 51; Indels Pred. No. 9.24e-147; 23.5%; 74.0%; Matches 145; Conservative Best Local Similarity Query Match

43 atggactggacctggagcatcctttnttggtggcagcagcaacaggtgcccactcccag 102 අ ð

1 ATGGGATGGAGCGGGATCTTTCTCTTCTGTCAGGAACTGCAGGTGTCCACTCTGAG 60

103 gttcagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcc 162 염

61 ATCCAGCTGCAGCAGCTCTGGACCTGATGAAGCCTGGGGCTTCAGTGAAGATATCC 120 ð

163 tgcaaggcttctggttacacctttaccagctacggtatcagctgggtgcgacaggcccct 222 쇰

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ggacaagggcttgagt 238 223 유

standard; RNA; EST; 209 BP. HS93811

T28938;

08-JAN-1995 (Rel. 42, Created) 07-SEP-1995 (Rel. 45, Last updated, Version 2) EST61186 Homo sapiens cDNA 5' end similar to immunoglobulin mu heavy chain, VDJ regions (GB:M17751) (HT:3055).

Homo sapiens (human)

Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae

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Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A.,

An Bult C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D.,
An Bult C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D.,
An Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D.,
A FitzGeard L.M., FitzHugh W.M., Fritchman J.L., Geoghagen N.S.M.,
A Glodek A., Gnehm C.L., Hanna M.C., Heddlom E., Hinkle Jr P.S.,
A Merick J.M., MORENO-PALANQUES R.F., McDonald L.A., Nguyen D.T.,
Pellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L.,
A Saudek D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R.,
A Gloman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A.,
A Fisten C., Hattings G.A., He W., Hu J.S., Greene J.M.,
A Fisten C., Hattings C.A., He W., Hu J.S., Greene J.M.,
A Meisener P.S., Olsen H., Raymond L., Weil Y.F., Wing J., Xu C.,
A Yungen J.M., Weillon P.J., Fannon M.R., Rosen C.A.,
A Weiler J., Hugson P., Kim A., Fannon M.R., Rosen C.A.,
A Weiler J., Weiler S.M., Dillon P.J., Fannon M.R., Rosen C.A.,

"Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence"; Haseltine W.A., Fields C., Fraser C.M., Venter J.C.;

Unpublished.

Contact: Venter, JC The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878 Tel: 3018699056 Fax: 3018699423 Email: tdbinfo@tdb.tigr.org For clone availability, additional sequence

and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org). NCBI gi: 611036

Location/Qualifiers

US-08-137-117B-26 rat Jul 8 08:37

/organism="Homo sapiens"

/note="human" <1..>209

Sequence 209 BP; 43 A; 62 C; 48 G; 55 T; 1 other; mRNA

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Gaps .; 0 Length 209; 0; Mismatches 56; Indels Score 88; DB 125; Pred. No. 9.47e-132; 21.7**%;** 71.9**%**; Best Local Similarity 71.9%; Matches 143; Conservative Query Match

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62 3 gatgintcoctggtaatggtgactctgcoctggaacttctgtaaatattttggttacca

281 GATTIGICAACAGICAAIGIGGCCTIGCCCTIGAAITICIGGIIGIAGCIAGIACCACCA 222

63 ttgccagcgttgatccatcccatccactcaagcctttgtccgggggcctggcgcacccaa 122

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EST61186 Homo sapiens cDNA 5' end similar to immunoglobulin mu 06-SEP-1995 EST mRNA 209 bp T28938 ڡ DEFINITION RESULT

heavy chain, VDJ regions (GB:M17751) (HT:3055) T28938 ACCESSION KEYWORDS

human primer=M13 Reverse library=Human White blood cells.

Homo sapiens ORGANISM

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 209) REFERENCE AUTHORS

Bult C.J., Lee, N. Tirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W., Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., FitzGerald, L.M., FitzHugh, M.M., Fritchman, J.L., Geoghagen, N.S.M., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr.P.S., Kelley, J.M., Klimek, K.M., Kelley, J.C., Liu, L.-I., Marnaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nquyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Collins, E.-J., Dinke, D., Feng, P., Ferrie, A., Fischer, C., Hastings, G.A., He, M.-H., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., L Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C. JOURNAL

TITLE

Contact: Venter, JC

The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878

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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pI773 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares R86288 385 bp mRNA EST 14-AUG-1995 ypl2e09.rl Homo sapiens cDNA clone 187240 5' similar to gb:L02325 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN); Email: tdbinfo@tdb.tigr.org For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database ö Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI Adult human. 281 GATTIGICAACAGICAATGIGGCCTIGCCCTICAATTICIGGIIGIAGCIAGIACCACCA 222 63 ttgccagcgttgatccatccatccactcaagcctttgtccggggggcctggcgcacccaa 122 221 ITGAAAGGAICAATATATCCAATCCACTCAAGGCTCTTTCCATGCCTCTGCTTCACCCAG 162 123 tgcatagcatagctagtgaaggtgtatccagaagccttgcaggaaaccttcactgaggcc 182 human clone=187240 library=Soares breast 3NbHBst vector=pT7T3D Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; 3 gatgintccctggtaatggtgactctgccctggaactictgtaaatattitgtgttacca 62 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Gaps Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 385) ; Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Length 209; 1 others 0; Mismatches 56; Indels Score 88; DB 70; LA Pred. No. 9.47e-132; 55 t /organism="Homo sapiens" /note="human" Location/Qualifiers δ 48 (tdbinfo@tdb.tigr.org) 183 ccaggettetteaceteag 201 and M.Fatima Bonaldo. 101 CCAGGCTTCATCAGCTCAG 83 Query Match 21.7%; Best Local Similarity 71.9%; 62 c 143; Conservative <1..>209 1..209 NCBI gi: 611036 Tel: 3018699056 Fax: 3018699423 Homo sapiens 43 a Wilson, R. R86288 source DEFINITION ORGANISM BASE COUNT Matches **PRNA** ACCESSION REFERENCE AUTHORS FEATURES KEYWORDS SOURCE ORIGIN LOCUS 용 ც g g ප g ე g

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Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldher, R.A.,
Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W.,
Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hudhes, J., Finch, L.D.,
FitzGerald, L.M., FitzHugh, W.M., FitzChman, J.L., Geodhagen, N.S.M.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr, P.S., Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; IMAGE Consortium (info@image.llnl.gov) for further information. This clone is available royalty-free through LLNL; contact the 127 ctgaggtgaagatgcctggggcctcagtgaagctttcctgcaaggcatctggattcgcgc 186 187 tcaqccaccactacatgcactgggtgcgacaggcccctgggacaagggattnagtggctg 246 T27727 29 bp mRNA EST 06-SEP-1995 EST13874 Homo sapiens cDNA 5' end similar to immunoglobulin mu (gamma) heavy chain, V(IV)DJC regions (HT:3057). 67 tetgettgetggetgtagetecaggtgeteacteceaggtgeaggtngtgeagtetgggg 126 83 CTGAGCTGATGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGGTTACTCAT 142 143 TCACTAGCTATTACATACACTGGGTGAAGCAGCCATGGAAAGAGCC-TTGAGTGGATT 201 23 TCTTCCTTCTGTCAGGAACTGCAGGTGTCCACTCTGAGATCCAGCTGCAGCTGTGGAC 82 Gaps Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 1; Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Score 72; DB 58; Length 385, 6 others 0; Mismatches 53; Indels human primer=M13 Reverse library=Human Testis. Pred. No. 4.76e-98; u 18 /organism="Homo sapiens"/clone="187240" Email: est@watson.wustl.edu High quality sequence stops: 323 Source: IMAGE Consortium, LINL 112 g Location/Qualifiers The WashU-Merck EST Project = = = = = = WashU-Merck EST Project /note="human" 299 bp Query Match 17.8%; Best Local Similarity 70.5%; 104 c (bases 1 to 299) 129; Conservative Contact: Wilson RK Unpublished (1995) 1..385 NCBI gi: 944694 Homo sabiens æ 82 247 gga 249 204 = 85 = 85 œ source BASE COUNT ORIGIN DEFINITION ORGANISM Matches TITLE JOURNAL 202 ACCESSION REFERENCE AUTHORS KEYWORDS FEATURES SOURCE LOCUS 쇰 g 쇰 ð g Š δ ð

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Coleman T.A., Collins E.J., Dimke D., Feng P., Ferrie A.,
Fischer C., Hastings G.A., He W.W., Hu J.S., Greene J.M.,
Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li H., Contact: Venter, JC The Institute for Genomic Research 932 Clopper and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org). NCBI gi: 609825 35 ggttetteetteteetggtggeageteecagatgggteetgteecaggtgeagetgeagg Rd, Gaithersburg, MD 20878 Tel: 3018699056 Fax: 3018699423 Email: tdbinfoetdb.tigr.org For clone availability, additional sequence S.scrofa mRNA; expressed sequence tag (5'; clone c1d10). F14516 Meissner P.S., Olsen H., Raymond L., Wei Y.F., Wing J., Xu C., Yu G.L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A., Haseltine W.A., Fields C., Fraser C.M., Venter J.C.; "Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence"; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae Vertebrata; Mammalia; Score 54; DB 127; Length 299; Pred. No. 1.35e-61; 0; Mismatches 71; Indels Sequence 299 BP; 61 A; 84 C; 82 G; 68 T; 4 other; /organism="Homo sapiens" /note="human" Chordata; Location/Qualifiers RNA Animalia; Metazoa; 13.3**%**; 63.8**%**; 330 bp 125; Conservative 215 agtggattgggtatat 230 194 AGTGGATTGGATATAT 209 <1..>299 Best Local Similarity SSC1D10 Unpublished. Eukaryota; Query Match 10 DEFINITION ACCESSION KEYWORDS source Matches 1 - 299LOCUS 셤 셤 셤 8 δ 유 δ à Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Heidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A., Fischer, C., Hastings, C.A., He, W.-W., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Meissner, P.S., Oleen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Hasettine, W.A., Fields, C., Fraser, C.M., and Venter, J.C. Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of CDNA Sequence Email: tdbinfoëtdb.tigr.org For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database ö Klimek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., agtcgggcccaggactggtgaagccttcggagaccctgtccctcacctgcactgtctctg 154 gtggctccatcagtagttactactggagctggatccggcagccccagggaagggactgc 214 GTTACTCATTCACTAGCTATTACATACACTGGGTGAAGCAGAGGCCATGGAAAGAGCCTTG 193 14 GGATCTTTCTTCTTCTTCTTCTGTCAGGAAACTGCAGGTGTCCACTCTGAGAATCCAGCTGCAGC 73 35 ggttcttccttctcctggtggcagctcccagatgggtcctgtcccaggtgcagctgcagg 94 0; Gaps EST13874 Homo sapiens cDNA 5' end similar to immunoglobulin mu (qamma) heavy chain, V(IV) DJC regions (HT:3057). Score 54; DB 69; Length 299; Pred. No. 1.35e-61; 0; Mismatches 71; Indels 4 others 12-JAN-1995 (Rel. 42, Created) 07-SEP-1995 (Rel. 45, Last updated, Version 2) EST13874 Homo sapiens cDNA 5' end similar to in 932 Clopper Rd, Gaithersburg, MD 20878 ų 89 The Institute for Genomic Research /organism≂"Homo sapiens" .r 9 HST27727 standard; RNA; EST; 299 BP. Location/Qualifiers Б 82 (tdbinfo@tdb.tigr.org). /note="human" / Match 13.3%; Local Similarity 63.8%; Contact: Venter, JC 84 c 125; Conservative 194 AGTGGATTGGATATAT 209 215 agtggattgggtatat 230 Unpublished (1995) <1..>299 1..299 Tel: 3018699056 Fax: 3018699423 MCBI gi: 609825 Homo sapiens (human)

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Submitted (26-JUL-1995) to the EMBL/GenBank/DDBJ databases.
Winteroe A.K., The Royal Veterinary and Agricultural University,
Department of Animal Science and Animal Health, Division of Animal
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Evaluation and characterization of a porcine small intestine cDNA
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                             Eukaryotae; mitochondrial eukaryotee; Metazoa; Chordata;
Vertebrata; Sarcopterygii; Mammalia; Eutheria; Artiodactyla;
Suiformee; Suina; Suidae; Sus.
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77 c 104 g 76 t 2 others
                                                                                                                                                                                                                                                      Genetics, Bulowsvej 13, 1870 Frederiksberg C, DENMARK
NCBI gi: 971726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 51; DB 64; Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 117; Indels
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30-AUG-1995 (Rel. 45, Last updated, Version 1)
                                                                                                                                                                                                                                                                                                                                                                                                        /note="expressed sequence tag
                                                                                                                                                                                                                                                                                                                        /organism="Sus scrofa"
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                                                                                                                                                                                                                                                                                          Location/Qualifiers
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Best Local Similarity 58.7%;
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human clone-81635 library-Stratagene lung (#937210)
vector=pBluescript SK- host=SOLR cells (kanamycin resistant)
primer=M13RP1 Rsitel=EcoR1 Rsite2=XhoI Normal lung tissue from a 72
year old male. Cloned unidirectionally. Primer: Oligo dT. Average ö yc24f06.rl Homo sapiens cDNA clone 81635 5' similar to gb:M18512 HEAVY CHAIN PRECURSOR V-I REGION (HUMAN); /tissue type="small intestine" /clone lib="directionally cloned cDNA in XL1-blue MRF'" /clone="cld10" 165 ggtccgccaggctccagggaaggggctggagtggctggcggctattagtactagtcgtgg 224 105 gtctctgagactctcctgtgtcggctctggattcaccttcagtggtacctacattaactg 164 45 aggtgtccagggtgaggagaaggtggtggagtctggaggaggcctggtgcagcctgggng 104 45 AGGTGTCCACTCTGAGATCCAGCTGCAGCAGTCTGACCTGAGCTGATGAAGCCTGGGGGC 104 165 GGTGAAGCAGAGCCATGGAAAGAGCCTTGAGTGGATTGGATATATTGATCCTTTCAATGG 224 tagtacctactacacagactctgtggagggccgattcaccatctccaaagacaactccca 284 225 TGGTACTAGCTACAACCAGAAATTCAAGGGCAAGGCCACATTGACTGTTGACAAATCTTC 284 20-FEB-1995 Gaps Winteroe A.K., The Royal Veterinary and Agricultural University, Department of Animal Science and Animal Health, Division of Animal Genetics, Bulowsvej 13, 1870 Frederiksberg C, DENMARK "Evaluation and characterization of a porcine small intestine cDNA ; 0 Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Artiodactyla; Suiformes; Suidae. /product="Ig heavy chain variable VDJ region" Submitted (26-JUL-1995) to the EMBL/GenBank/DDBJ databases. Length 330; 0; Mismatches 117; Indels 285 gaagacggcctatctgcaaatnaacagcctgagaacagaagac 327 285 CAGCACAGCCTACATGCATCTCAGCAGCCTGACATCTGAGGAC 327 EST /note="expressed sequence tag" 71 A; 77 C; 104 G; 76 T; 2 other; Score 51; DB 129; Pred. No. 9.76e-56; = = = = = Winteroe A.K., Fredholm M., Davies W.; /organism="Sus scrofa" mRNA Location/Qualifiers 169 bp Query Match 12.6%; Best Local Similarity 58.7%; 166; Conservative /partial 1.,>330 BP. Winteroe A.K.; T64512 T64512 Sequence 330 EST. Unpublished. library" V_region 15 source DEFINITION 1 - 3301 - 330Matches 522 ACCESSION KEYWORDS RESULT

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US-08-137-117B-26 rst

Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; ypl1g03.r1 Homo sapiens cDNA clone 187156 5' similar to gb:M62726 IG HEAVY CHAIN V-III REGION (HUMAN); 2; High qality sequence stops: 139 Source: IMAGE Consortium, LIANL This clone is available royalty-free through LIANL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), 102 gtgcgcctggtgcagtctggggctgagatgaggaagcctgggcct-cagtgaaggtctcc 160 61 ATCCAGCTGCAGCTCTGGACCTGAGCTGAAGCCTGGGGCTTCAGTGAAGATATCC 120 human clone=187156 library=Soares breast 3NbHBst vector=pT7T3D 43 atggactggacctggaggatcctcttcttggtggcagtagcaagnga-gcccactcccag 101 Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. Wash U-Werck, EST Project 1 ATGGGATGGAGCGGGATCTTTCTCTTCTTCTGTCAGGAACTGCAGGTGTCCACTCTGAG 60 04-AUG-1995 Gaps adaptor sequence 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 5; Length 169; 1 others 0; Mismatches 36; Indels Eutheria; Primates; Catarrhini; Hominidae; Homo. insert size: 1.0 kb; Uni-ZAP XR Vector; 5' 5'-GAATTCGCCACGAG-3'; 3' adaptor sequence: Washington University School of Medicine Score 43; DB 79; Pred. No. 1.53e-40; 36 t /organism="Homo sapiens" 5'-crccagttrtttttttttttt-3' mRNA Location/Qualifiers 5 Email: est@watson.wustl.edu 52 Contact: Wilson RK WashU-Merck EST Project /clone="81635" /note="human 303 bp 10.6%; 70.3%; 49 c (bases 1 to 169) 90; Conservative Unpublished (1995) NCBI gi: 673557 Best Local Similarity Homo sapiens 121 TGCAAGGC 128 161 tgccaggc 168 ø 31 R83139 R83139 Query Match Source RESULT 13 DEFINITION COUNT ORGANISM Matches TITLE JOURNAL **ACCESSION** REFERENCE AUTHORS FEATURES KEYWORDS COMMENT SOURCE ORIGIN BASE 염 음 ð 임 ð ð

human clone-21441 primer=M13RP1 library-Soares fetal liver spleen INFLS vector=pT7T3D (Pharmacia) with a modified polylinker

mRNA EST 31-0CT-1995 CDNA clone 214441 5' similar to 9b:M62726

ys11b01.r1 Homo sapiens cDNA clone 21' IG HEAVY CHAIN V-III REGION (HUMAN);.

419 bp

H73816

DEFINITION

ACCESSION KEYWORDS

SOURCE

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DB 57; Length 303; 63; Indels

Pred. No. 1.53e-40;

Score 43;

10.6%; 61.8%;

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102; Conservative

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Best Local Similarity

Query Match

9 others

76 t

65 c

62

BASE COUNT

45 AGGTGTCCACTCTGAGATCCAGCTGCAGAGTCTGGACCTGAGCTGATGAAGCCTGGGGC 104

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98 aggtgtccagtgtcaggtgcagctggaggagtctggggggaggcgtggtccagcctgggag 157

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digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 303)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; WashU-Merck EST Project Washington University School of Medicine /organism="Homo sapiens" High quality sequence stops: 111 Source: IMAGE Consortium, LLNL 91 g Location/Qualifiers The WashU-Merck EST Project Email: est@watson.wustl.edu /clone="187156" /note="human" and M.Fatima Bonaldo Contact: Wilson RK Unpublished (1995) Tel: 314 286 1800 Fax: 314 286 1810 1..303 NCBI gi: 928016 Homo sapiens Wilson, R. source ORGANISM AUTHORS REFERENCE FEATURES

I and cloned into the Pac I and Eco RI sites of the modified pTTT3 vector. Library went through one round of normalization. Library Deuterostomia, Chordata, Vertebrata, Gnathostomata, Osteichthyes, Sarcopterygii, Choanata, Tetrapoda, Amniota, Mammalia, Theria, Eutheria, Archonta, Primates, Catarrhini, Hominidae, Homo. ö This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. 266 206 277 278 AATCTICCAGCACAGCCTACAIGCAICICCAGCAGCCIGACAICIGAGGACICIGCAGICI 337 ctgggggggtccctgagactctcctgtgcagcgtctggattcaccttcagtagctatggca 86 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Gaps 147 atggaagtaataaatactatgcagactccgtgaagggccgattcaccatctccagagaca 218 TCAATGGTGGTACTAGCTACAACCAGAAATTCAAGGGCAAGGCCACATTGACTGTTGACA 207 attccaagaacacgctgtatctgcaaatgaacagcctgagagctgaggacacggctgtgt Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 .; 0 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Score 43; DB 100; Length 419; 0; Mismatches 103; Indels 10 others constructed by Bento Soares and M.Fatima Bonaldo. Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine Pred. No. 1.53e-40; ų 102 /organism="Homo sapiens" /clone="214441" High quality sequence stops: 261 Source: IMAGE Consortium, LINL Location/Qualifiers 116 g Email: est@watson.wustl.edu The WashU-Merck EST Project /note="human" 10.6%; 100 c Best Local Similarity 58.6%; (bases 1 to 419) 146; Conservative Unpublished (1995) <1..>419 NCBI gi: 1046750 1..419Homo sapiens Wilson, R. 91 Query Match source ORGANISM TITLE BASE COUNT mRNA 27 86 Matches REFERENCE AUTHORS FEATURES ORIGIN 염 염 셤 g ð ð ₽ δ

206 207 attecaagaacaegetgtatetgeaaatgaacageetgagagetgaggaeaeggetgtgt 266 218 TCAATGGTGGTACTAGATACAACCAGAAATTCAAGGGCAAGGCCACATTGACTGTTGACA 277 27 ctggggggtccctgagactctcctgtgcagcgtctggattcaccttcagtagctatggca 86 Gaps Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.; "The WashU-Merck EST Project"; est@watson.wustl.edu High quality sequence stops: 261 Source: IMAGE Consortium, LINL This clone is available royalty-free through LINL 147 atggaagtaataaatactatgcagactccgtgaagggccgattcaccatctccagagaca 03-NOV-1995 (Rel. 45, Created)
03-NOV-1995 (Rel. 45, Last updated, Version 1)
ysllb01.rl Homo sapiens cDNA clone 214441 5' similar to qb:M62726
IG HEAVY CHAIN V-III REGION (HUMAN); Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: contact the IMAGE Consortium (info@image.llnl.gov) for further ;; 0 Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Query Match 10.6%; Score 43; DB 124; Length 419; Best Local Similarity 58.6%; Pred. No. 1.53e-40; 0; Mismatches 103; Indels Sequence 419 BP; 91 A; 100 C; 116 G; 102 T; 10 other; US-08-137-117B-26 rat /organism="Homo sapiens" RNA; EST; 419 BP Location/Qualifiers /clone="214441" /note="human" Ξ information. NCBI gi: 1046750 146; Conservative <1..>419 LT 15 HS816226 standard; Homo sapiens (human) attactgtg 275 338 ATTACTGTG 346 attactgtg Unpublished. H73816; source Jul 8 08:37 1 - 419Matches 267 267 RESULT g g 염 ð අ g ð ð 염 ð ò

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338 ATTACTGTG 346

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Jul 8 08:37

Search completed: Mon Jul 8 08:47:49 1996 Job time: 199 secs.

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Jul 8 08:20

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Materman algorithm

Mon Jul 8 08:30:11 1996; MasPar time 7.52 Seconds 453.526 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-137-117B-27 (1-135) from USO8137117B.pep 989 Title:

Description: Perfect Score:

1 MGWSGIFLFLLSGTAGVHSE......ARGGNRFAYWGQGTLVTVSA 135 Sequence:

PAM 150 Gap 11 Scoring table:

82306 seqs, 25270970 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

1:ann 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4 8:unann5 9:unann6 10:unann7 11:unann8 12:unrev1 13:unrev2 Mean 40.986; Variance 126.476; scale 0.324 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

:	Š.	-89	68-	-84	-84	-83	-82	-82	98-	8	-79	-79	-78
	Pred. No	-	8.44e - 89		7.67e-84			•	3.13e - 80	4.25e-80		3.66e-79	7.92e-78
:	Description	Ig heavy chain precu	Ig heavy chain precu	Iq qamma-2b chain -	Ig heavy chain precu	Ig heavy chain V reg	Iq heavy chain precu	anti-digoxin transfe	Ig heavy chain precu	Iq heavy chain V req	Ig heavy chain precu	Ig heavy chain precu	Ig gamma-2a chain -
	TD	н32513	PS0057	\$25057	A27609	521810	HVMS8A	PH0105	A30577	PN0444	JL0076	PL0011	S37483
1	2	2	S	13	2	S	7	13	S	Ŋ	2	S	11
:	atch Length DB	137	135	474	139	138	117	138	135	150	141	151	469
Query	Match	81.8	81.7	78.6	78.0	77.8	77.0	76.9	75.2	75.1	74.8	74.4	73.4
	Score	808	808	777	111	169	162	761	744	743	740	736	726
Result	. No.	-	7	3	4	2	9	7	0 0	6	10	Ξ	12

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	38 675 6 40 675 6 41 673 6 42 673 6 43 673 6 44 673 6

ALI GNMENTS

- mouse se mouse ftext_change	ohnson, M.E.; .; Theofilopoulos,	region gene complex coding anti-DNA	immunoglobulin homology #checksum 816	l37; ls 2; Gaps 2;
H32513 #type complete Ig heavy chain precursor V region (BXM16) - mouse fformal name Mus musculus #common_name house mouse 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 12.Apr-1995	H32513 A94689 Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.; Dixon, F.J.; Theofilopoulos, A.N.	J. Clin. Invest. (1988) 82:852-860 Immunoglobulin kappa light chain variable region gene complex organization and immunoglobulin genes encoding anti-DNA autoantibodies in lupus mice. es MUD:8831394	bulin V region; r-weight 15108	Score 809; DB 5; Length 137; Pred. No. 6.20e-89; 13; Mismatches 9; Indels 2; Gaps 2;
H32513 #type of the control of the c	H32513 A94689 Kofler, R.; Stroha Noonan, D.J.; Du A.N.	<pre># fournal J. Clin. Invest. (1988) 82:852-860 #title Immunoglobulin kappa light chain v.</pre>	cession H32513 ##molecule_type_DNA ##residues 1-137 ##label KOF FICATION #euperfamily immunoglol Y #length 137 #molecular	Query Match 81.8%; Sc Best Local Similarity 82.5%; Pr Matches 113; Conservative 1:
RESULT 1 ENTRY TITLE ORGANISM DATE	ACCESSIONS REFERENCE #authors	<pre># journal #title #cross-refer</pre>	#accession ##molecule ##residues CLASSIFICATION SUMMARY	Query Match Best Local Si Matches 113

1 mgwswiflfllsvtagvhseiqlqqsgaelvkpgasvkisckasgysftgynmnwvkqsh 60

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#superfamily immunoglobulin V region; immunoglobulin homology the authors translated the codon AAG for residue 32 as The gene encoding this protein was isolated from a hybridoma that $gkslewigrinpyngdtfyngkfkgkatltvdkssstahmelrsltsedsavyycarlny\ 120$ 61 GKSLEWIGYIDPFNGGTSYNQKFKGKATLTVDKSSSTAYMHLSSLTSEDSAVYYCAR-G-118 Biased expression of variable region gene families of the 61 gkølewigninpyygstsyngkfkgkatltvdkssstaymqlnsltsedsavyycarkny 120 Ig gamma-2b chain - mouse #formal name Mus musculus #common name house mouse 25-Feb-1994 #sequence_revision 25-Feb-1994 #text_change 25-Feb-1994 Gapa Ig heavy chain precursor V region (PAR) - mouse #formal name Mus musculus #common name house mouse 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change Yaoita, Y.; Takahashi, M.; Azuma, C.; Kanai, Y.; Honjo, immunoglobulin heavy chain in autoimmune-prone mice. 1 mgwswiflfllsvtagvfsevqlqqsgpelvkpgasvkisckasgysftgyfmnwvkqsh #domain signal sequence flabel SIG\
#product Ig V region PAR flabel MAT
#length 135 #molecular-weight 15019 #checksum 5383 ; 81.7%; Score 808; DB 5; Length 135; 8; Mismatches 13; Indels produces anti-poly (ADP-ribose) antibody Pred. No. 8.44e-89; Asn and GAC for 92 as Gly J. Biochem. (1988) 104:337-343 #type complete 1-135 ##label YAO ##cross-references GB:D00307 fcross-references MUID:89197817 immunoglobulin Best Local Similarity 84.4%; 119 GNRFAYWGQGTLVTVSA 135 121 gssfdywgqgttltvss 137 12-Apr-1995 114; Conservative 121 rgaywgggtlvtvsa 135 ##molecule_type DNA PS0057 PS0057 PS0057 #residues CLASSIFICATION *accession Query Match #note m Jul 8 08:20 ~ #authors journal ACCESS IONS ACCESS IONS 121 61 20-135 Matches TITLE ORGANISM REFERENCE title ORGANISM COMMENT KEYWORDS FEATURE 1-19 SUMMARY RESULT ENTRY TITLE ENTRY DATE 쇰 ð g à 유 ò 요 엄 ð 8 8

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##residues ##status accession #authors journal 🕯 ACCESSIONS #title TITLE ORGANISM DATE 20-117 34 - 117REFERENCE ORGANISM SUMMARY FEATURE 1 - 19SUMMARY RESULT ENTRY ENTRY TITLE 셤 염 δ g 염 δ ð δ δ ##note the sequence was determined from the germline gene CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology #superfamily immunoglobulin V region; immunoglobulin homology #length 138 #molecular-weight 15258 #checksum 1535 Ig 5; Ostermeyer, M.; Brack, C.H.; Traunecker, A.; Koehler, G. submitted to the EMBL Data Library, January 1991 Nucleotide sequence of a rearranged VDJ-region of a mouse 61 GKSLEMICYIDPFNGGTSYNQKFKGKATLTVDKSSSTAYMILSSLTSEDSAVYYCARG-G 119 61 ggglewigwiypgnvntkynekfkgkatltadkssstaymqlssltsedsavyfcarnyg 120 61 GKSLEWIGYIDPFNGGTSYNQKFKGKATLTVDKSSSTAYMHLSSLTSEDSAVYYCARGGN 120 Gaps Ig heavy chain precursor V region (108A) - mouse #formal name Mus musculus #common name house mouse 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change <u>.</u> Givol, D.; Zakut, R.; Effron, K.; Rechavi, G.; Ram, 3; #title Diversity of germ-line immunoglobulin V-H genes. #cross-references MUID:81245215 Length 138; mu heavy chain gene and its upstream region. 11; Mismatches 16; Indels Score 769; DB 5; 1 Pred. No. 1.42e-83; Nature (1981) 292:426-430 #type complete 1-117 ##label GIV 1-138 ##label OST ##cross-references EMBL:X56936 preliminary 121 ysyyamdywgggtsvtvss 139 121 -RF-A--YWGQGTLVTVSA 135 Query Match 77.8%; Best Local Similarity 78.3%; 121 ssyglaywgqgtlvtvsa 138 120 NRF--AYWGQGTLVTVSA 135 108; Conservative 23-Mar-1995 12-Apr-1995 Cohen, J.B. ##molecule_type DNA ##molecule_type DNA HVMS8A \$21810 521810 A02041 A02041 \$21810 15/3 ##residues description ##residues CLASSIFICATION submission ##status #accession accession Query Match #authors fintrons # journal #authors Matches ACCESSIONS ACCESSIONS TITLE REFERENCE REFERENCE ORGANISM GENETICS SUMMARY RESULT ENTRY ENTRY 염 ð 용 ò 셤 8 à 셤 à

an 5; Ig heavy chain precursor V region (MRL10) - mouse (fragment) #formal name Mus musculus #common name house mouse 04-May-1989 #sequence_revision 04-May-1989 #text_change ö Near, R.I.; Ng, S.C.; Mudgett-Hunter, M.; Hudson, N.W.; Margolies, M.N.; Seidman, J.G.; Haber, E.; Jacobson, M.A. Mol. Immunol. (1990) 27:901-909 fdomain signal sequence #status predicted #label SIG\ in 61 GKSLEWICKIDPPNGGTSYNQKFKGKATLYVDKSSSTAYMHLSSLTSEDSAVYYCA-RGC 119 61 gksldyigyispysgvtgynqkfkgkatltvdkssstaymelrsltsedsavyycagssg 120 09 1 mgwswiflfllsgtagvhsevqlqqsgpelvkpgasvkisckasgytftdynmhwvkqsh 60 1 MGWSGIFLFLLSGTAGVHSEIQLQQSGPELMKPGASVKISCKASGYSFTSYYIHWVKQSH 60 Gaps Gaps PH0105 #type fragment anti-digoxin transfectoma antibody light chain V region #formal name Mus musculus #common name house mouse 21-Nov-1993 #sequence_revision 21-Nov-1993 #text_change 61 gkslewigyiypynggtgyngkfkskatltvdnssstaymelssltsedsavyycar 117 Heavy and light chain contributions to antigen binding 61 GKSLEWIGYIDPENGGISYNQKFKGKATLIVDKSSSTAYMHLSSLISEDSAVYYCAR 117 $1\ \mathtt{mgwswiflfll} sgtagvlsevqlqqsgpelvkpgasvrmsckssgyiftdfymnwvrqsh$ produced by anti-digoxin chain recombinant antibody produced by transfection of cloned anti-digoxin antibody genes. #cross-references MUID:91015092 #product Ig heavy chain V region (108A) #status
predicted #label MAT\ ; ; .; 0 #domain immunoglobulin homology #label IMM #length 117 #molecular-weight 12971 #checksum Length 138; Indels Length 117; Indels Query Match 77.0%; Score 762; DB 2; Ler Best Local Similarity 88.9%; Pred. No. 1.23e-82; Matches 104; Conservative 8; Mismatches 5; 18; Mismatches 12; Score 761; DB 13; Pred. No. 1.67e-82; precursor - mouse (fragment) 1-138 ##label NEA #length 138 #checksum 3011 #type fragment preliminary 121 nkwamdywqhqasvtvss 138 |: | |||:|: ||||: | 120 NRFA--YWGQGTLVTVSA 135 Query Match 76.9%; Best Local Similarity 76.1%; Matches 105; Conservative 21-Nov-1993 12-Apr-1995 A30577 PH0105 PH0105 PH0105

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#superfamily immunoglobulin V region; immunoglobulin homology specific for a different antigen (phOxazolone, NP or GAT). PL0011 #type fragment
Ig heavy chain precursor V region (4C11) - mouse (fragment)
#formal name Mus musculus #common name house mouse
30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change Kaartinen, M.; Rocca-Serra, J.; Maekelae, 0.
Mol. Immunol. (1988) 25:859-865
Combinatorial association of V genes: one VH gene codes for #product Ig heavy chain #status predicted #label MAT\
fregion complementarity-determining 1\
fregion complementarity-determining 2\ 61 grglewigridpnsggtkynekfkskatltvdkpsstaymglssltsedsavyycaregp 120 61 GKSLEWIGYIDP-FNGGISYNQKFKGKATLIVDKSSSTAYMHLSSLISEDSAVYYCARGG 119 61 gkslewigdidpnfds-ssynqkfkgkatltvdkssntaymelrsltsedtavyycargg 119 3 1g heavy chain precursor V region (anti-phenyloxazolone, 18C10) - mouse (fragment) Gaps #formal name Mus musculus #common name house mouse 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 1 mewswiflfllsgtagvlsevqlqqfgaelvkpgtsvkisckasgyiftdynmdwvkqsh three non-cross-reactive monoclonal antibodies each ö 74.8%; Score 740; DB 5; Length 141; 73.3%; Pred. No. 1.07e-79; 20; Mismatches 16; Indels #domain signal sequence #label SIG\ #length 141 #checksum 8784 #type fragment fregion J2 segment/ 1-141 ##label KAA Best Local Similarity 73.3%; 120 fpygmdywgqgtsvtvss 137 120 NRFA--YWGOGTLVTVSA 135 fregion C 99; Conservative 12-Apr-1995 JL0076 121 agdywgggttltvss 135 121 RFAYWGQGTLVTVSA 135 ##molecule_type mRNA JI0076 JL0076##residues CLASSIFICATION Query Match #accession 1 2

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NN #superfamily immunoglobulin V region; immunoglobulin homology
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                                                                                                           Structural basis of stimulatory anti-idiotypic antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 gkslewiggfdpnydntfynekfkdkatltvdkssttaymelrsltsedsavyycasydy 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
                                                     Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 mgwswiflfllsgtagvlsevqlqqsgpellkpgasvkisckasgytftdytmhwvkqsh
                                                                                                                                                                                   ##residues 1-151 ##label CHE
##experimental source cell line 4C11
This protein is an anti-idiotypic antibody that induces an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #length 469 #molecular-weight 51549 #checksum 7833
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submitted to the EMBL Data Library, February 1993
837483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 74.4%; Score 736; DB 5; Length 151.
Best Local Similarity 77.9%; Pred. No. 3.66e-79;
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fregion complementarity-determining 2/
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fromain constant region flabel COR
flength 151 fchecksum 2479
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                                                                                          Mol. Immunol. (1988) 25:33-40
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120 NRFAYWGQGTLVTVSA 135
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28-Apr-1995
                                                                          Kohler, H.
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ä Sassano, M.; Repetto, M.; Cassani, G.; Corti, A. submitted to the EMBL Data Library, January 1994
PCR amplification of antibody variable regions with primers Ig heavy chain precursor V region (F6-3) - mouse (fragment) #formal name Mus musculus #common name house mouse 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change Structural basis of stimulatory anti-idiotypic antibodies. 61 vrslewigrispyngvtsynknfkdkatltvdessstaymelhsltsedsavyyctrptt 120 61 GKSLEWIGYIDPFNGGTSYNQKFKGKATLTVDKSSSTAYMHLSSLTSEDSAVYYCAR-GG 119 61 ggglkwigwiypasgntkynenfkgkatltvdtssstaymqlssltsedtavyfcaramg 120 9 1 MGWSGIFLFLLSGTAGVHSEIQLQQSGPELMKPGASVKISCKASGYSFTSYYIHWVKQSH 60 9 Gaps 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 03-Mar-1995 Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H. 1 mgwswififilagtagvisavqlqqsqpelvkpqasvkisckasqdsftgndlhwvrqsh #length 138 #molecular-weight 15208 #checksum 9990 3; Score 723; DB 11; Length 138; Pred. No. 1.99e-77; Indela 12; Mismatches 17; that anneal to constant regions Mol. Immunol. (1988) 25:33-40 #type fragment 1-138 ##label SAS 1-166 ##label CHE #cross-references EMBL:X77230 #cross-references MUID:88142863
#accession PL0012 : |||||| :|||: 120 NR---FAYWGQGTLVTVSA 135 preliminary 121 atatlldywgggttltvss 139 Query Match 73.1%; Best Local Similarity 76.8%; Matches 106; Conservative 121 vdtwfpywgqgtlvtvsa 138 120 -N-RFAYWGQGTLVTVSA 135 11-Apr-1995 ##molecule_type mRNA ##molecule_type mRNA PL0012 541429 PL0011 S41429 PL0012 ##residues ##residues #description #submission #accession 13 14 #authors | journal authors **ACCESSIONS** ACCESSIONS title REFERENCE REFERENCE ORGANISM

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121 wfpywgggtlvtvsa 135 121 RFAYWGQGTLVTVSA 135 g Š

Search completed: Mon Jul 8 08:30:40 1996

Job time : 29 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch pp

477.475 Million cell updates/sec Mon Jul 8 08:29:44 1996; MasPar time 4.34 Seconds

Tabular output not generated.

Title:

MGWSGIFLFLLSGTAGVHSE......ARGGNRFAYWGQGTLVTVSA 135 >US-08-137-117B-27 (1-135) from USO8137117B.pep 989 Description: Perfect Score:

PAM 150 Scoring table:

Sequence:

43470 seqs, 15335248 residues

Searched:

Listing first 45 summaries Minimum Match 0% Post-processing:

swiss-prot31
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8

Database:

scale 0.560 Mean 41.703; Variance 74.406; Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Pred.

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Description HV02 MOUSE HV11 MOUSE HV15 MOUSE HV48 MOUSE HV51 MOUSE HV12 MOUSE HV13 MOUSE HV52 MOUSE HV59 MOUSE MOUSE HV07 HV02 £ Query Match Length DB 1117 1139 1130 1136 1138 1117 1117 1117 72.7 71.4 71.4 71.3 70.6 68.9 68.5 68.3 68.3 68.3 68.3 67.2 Score 762 719 717 706 705 698 681 677 675 675 675 Š. Result

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	HAND	4 HV10	4 HV05	4 HV03	4 HV50	4 HV1G	4 HV1B	4 HV1C	4 HV01	4 HV00	4 HV17	4 HV46	4 HV01	4 HV16	4 HV60	4 HV40	4 HV37	4 HV02	4 HV55	4 HV3G	4 HV32	4 HV61	4 HV3I	4 HV3B	4 HV33	4 HV3C	4 HV30	4 HV47	4 HV01	4 HV3A	4 HV27	K 11111 A
444	111	1117	117	120	120	117	117	143	121	114	117	137	142	136	116	119	119	135	117	122	115	116	119	114	115	117	113	113	114	122	113	111
	0.70	65.8	65.5	59.5	58.3	57.6	57.2	51.8	51.0	49.7	46.1	46.0	44.4	44.2	43.1	42.9	42.9	42.7	42.6	42.3	42.2	42.2	42.1	42.0	41.9	41.8	41.7	41.5	41.5	41.5	41.4	V 1 V
	663	651	648	288	577	570	995	512	504	492	456	455	439	437	426	424	424	422	421	418	417	417	416	415	414	413	412	410	410	410	409	900
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ALI GNMENTS

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SEQUENCE FROM N.A.
81245215
GIVOL D., ZAKUT R., EFFRON K., RECHAVI G., RAM D., COHEN J.B.;
NATURE 292:426-430(1981).
PIR; A02041; HVBSA.
PIR; A02041; HVBSA.
IMMUNOGLOBULIN V REGION; SIGNAL.
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                                                                                                                                                      21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN PRECURSOR V REGION (108A).
                                                  117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 AA; 12972 MW; 81037 CN;
                                                       PRT;
                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                       MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUTHERIA; RODENTIA.
LT 1
HV14_MOUSE
P01758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
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RESULT 110 HV HV 110 HV HV 110 HV HV 110 HV
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l mgwswiflfllsgtagvhsevqlqqsgpelvkpgasvkisckasgytftdynmhwvkqsh 60

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HV04 MOUSE HV06 MOUSE

2.40e-134 6.93e-134 2.34e-131 3.96e-131 1.60e-129 1.21e-125 3.01e-124 3.01e-124 1.21e-125 5.81e-123

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Gaps

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PRT; 139 AA

STANDARD;

LT 2 HV07_MOUSE

EUTHERIA; RODENTIA, SEQUENCE FROM N.A.

STRAIN=C57BL/6;

81234548

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3, 61 grglewigridpnsggtkynekfkskatltvdkpsstaymqlssltsedsavyycarydy 120 χ, Gaps IG HEAVY CHAIN V REGION (B1-8 / 186-2). BALTIMORE D.; CELL 24:625-637(1981). -!- THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING -NTROPHENYL) ACETYL (WPB ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL) ACETYL (WPB BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY 4: MUS MUSCULUS (MOUSE). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; COMPLEMENTARITY-DETERMINING 1. Score 719; DB 4; Length 139; Pred. No. 2.40e-134; FRAMEWORK 2. COMPLEMENTARITY-DETERMINING 21; Mismatches 14; Indels 10175; PO175; PO

JH2 SEGMENT. BY SIMILARITY

FRAMEWORK 3. D SEGMENT.

139 49 49 68 68 1117 1124 1139 1115

20 20 50 55 69 86

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DOMAIN DOMAIN

DOMAIN

FRAMEWORK 1.

HSSP; P01810; 1JHL. IMMUNOGLOBULIN V REGION; SIGNAL.

SIGNAL

PIR; A02034; MHMS18.

ANTIBODIES

15419 MW; 118806 CN;

139 AA;

SEQUENCE

NON TER

DISULFID

72.78; 71.9%;

100; Conservative

Matches

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Best Local Similarity

Query Match

61 ggglewigyinpgngyinynekfkgkttltvdkssstaymqlrsltsedsavyfcarshy 120 1 mgwsfiflfllsvtagvhsevqlqqsgaelvragssvkmsckasgytftsyginwvkqrp 60 Gaps IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY; HYBRIDOMA; SIGNAL. ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL) ACETYL (NPB BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY BALTIMORE D.; CELL 24:625-637(1981). -!- THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING MUS MUSCULUS (MOUSE). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; RODENTIA. 5; EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; SIMS J., RABBITTS T.H., ESTESS P., SLAUGHTER C., TUCKER P.W., IG HEAVY CHAIN V REGION (93G7). IG HEAVY CHAIN V REGION (S43) Score 717; DB 4; Length 140; Pred. No. 6.93e-134; 19; Mismatches 13; Indels P01755, 21-JUL-1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 10, LAST SEQUENCE UPDATE) 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE) IG HEAVY CHAIN PRECURSOR V REGION (S43). 21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN PRECURSOR V REGION (93G7). 137 AA. 140 AA; 15514 MW; 116859 CN; PRT; SIGNAL. 121 yggsydfdywgqgtpltvss 140 118 -GGN-RFAYWGQGTLVTVSA 135 Query Match 72.5%; Best Local Similarity 73.6%; Matches 103; Conservative PIR; A02038; G2MS43. HSSP; P01772; 1FGV. IMMUNOGLOBULIN V REGION; SCIENCE 216:309-311(1982) STANDARD; 19 137 49 MUS MUSCULUS (MOUSE). PIR; A02028; HVMSG7 EUTHERIA; RODENTIA. HSSP; P01789; 6FAB. SEQUENCE FROM N.A. SEQUENCE FROM N.A. 2 2 ANTIBODIES) LT 4 HV11 MOUSE STRAIN=A/J; CAPRA J.D.; 82152818 SEQUENCE 81234548 NON TER CHAIN DOMAIN SIGNAL SIGNAL CHAIN RESULT 연 셤 g ð δ ð

FRAMEWORK 1.

140 AA.

PRT;

STANDARD;

LT 3 HV02_MOUSE P01746;

RESULT ID HV AC P0

|: | |||||| :|||: 119 -GNR-FAYWGQGTLVTVSA 135 121 ygssyfdywgggttltvss 139

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120 NRFANWGCGTLUTUSA 135 121 FILL	đ	121 nyfdywgggtiltyss 136
HAVA MOUSE STANDARD; PRT; 138 AA.	δλ	
23-CCT-1986 (REL. 02, CREATED) 23-CCT-1986 (REL. 02, LAST ESDENCE UPDATE) 10-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE) 10 HEAVY CRAIN PRECORSOR V REGION (TEPC 1017). BUND MUSCULDS (MOUSE). EUNGANYOTA, MATAZOA, CHORDATA, VERTEBRATA, TETRAPODA, MAMMALIA, EDTHERIA, RODENITA. 84248078 861248078 861248078 861248078 872033, HWST7. PROC. NATL. AGAD. SCI. U.S.A. 81:4164-4168 (1984). POWAIN 21 49 FRAMEWORK 2. DOMAIN 21 88 138 138 FRAMEWORK 3. DOMAIN 118 127 COMPLEMENTARITY-DETERMINING 3. DOMAIN 69 85 TRAMEMORY 4. NON TER 138 138 138 FRAMEWORK 4. NON TER 138 138 138 FRAMEWORK 4. PROSECUE 688; DB 4; Length 138; PROSECUENCE ASSTERYTHWYGNEH 111111111111111111111111111111111111	REST	6 WOUSE STANDARD; PRT; 138
10 - AUG-1992 (REL. 23, LAST ANNOTATION UPDATE) 10 - AUG-1992 (REL. 23, LAST ANNOTATION UPDATE) 10 - AUG-1992 (REL. 23, LAST ANNOTATION UPDATE) 10 - AUG-1992 (REL. 24, LAST ANNOTATION UPDATE) 10 - AUG-1002 (MOUSE) 11 12 13 14 14 14 14 14 14 14	DT TO	(REL. 02, CREAT (REL. 02, LAST
MUS MUSCUIJUS (MOUSE). EUKRANCOTA, METAZOA, CHORDATA, VERTEBRATA, TETRAPODA, MAMMALIA, EUTHERIA, RODENTIA. [1] SEQUENCE FROM N.A. 84248078 GILLIAM A.C., SHEN A., RICHARDS J.E., BLATTNER F.R., MUSHINSKI J.F. TUCKER P.W.; FUCKER P.W.; F	담임	RSOR V
EUTHERIA; RODENTIA. EUTHERIA; RODENTIA.	_ର ଚ	MUS MUSCULUS (MOUSE). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALLA;
SEQUENCE FROM N.A. SEQUENCE FROM N.A.	OC R	
TUCKER P.W.; TU	2 2 3	1.1 SEQUENCE FROM N.A. 84248918
PUCKERY N.T. PUCKERY N. PUCKERY N. PUCKERY N. PUCKERY N. PUCKERY N. PUCKERY N. PURPOC. NATL. A02033; HVMST7. PURPOC. NATL. A02033; HVMST7. PURPOC. NATL. A02033; HVMST7. PURPOC. A02033; HVMST7. A02033; HVMST8. A020335; HVMST8. A0203335; HVMST8. A020335; HVMST8. A0203335; HVMST8. A0203335; HVMST8. A0203	2 2 2	RICHARDS J.E., BLATTNER F.R., MUSHINSKI
PIR, A02033, HVMST7.	R 13	U.S.A.
IMMUNOGLOBULIN V REGION; SIGNAL. 20 CHAIN V REGION (TEPC 1017). 20 CHAIN V REGION; SIGNAL. 1 20 CHAIN V RECION (TEPC 1017). 21 49 FRAMEWORK 1. DOMAIN 20 54 COMPLEMENTARITY-DETERMINING 1. DOMAIN 55 68 FRAMEWORK 2. COMPLEMENTARITY-DETERMINING 2. DOMAIN 66 117 FRAMEWORK 3. COMPLEMENTARITY-DETERMINING 2. DOMAIN 128 138 FRAMEWORK 4. DISULED 41 115 BY SIMILARITY. ENGRIPHINING 3. DOMAIN 128 138 FRAMEWORK 4. DISULED 41 115 BY SIMILARITY. ENGRET 138 138 FRAMEWORK 4. DISULED 41 115 BY SIMILARITY. ENGRET 138 138 FRAMEWORK 4. DISULED 41 115 BY SIMILARITY. ENGRET 138 138 FRAMEWORK 4. 1060-129; Astches 94; Conservative 25; Mismatches 16; Indels 3; Gap 41 111	DR DR	02033; HVMST7. P01810; 1JHL.
CHAIN 1 20	₹ 5	
DOMAIN 21 49 FRAMEWORK 1.	I E	21 138 IG HEAVY
DOMAIN 50 34 COMPLEMENTALITI-DELEGRINING 1. DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2. DOMAIN 86 117 FRAMEWORK 3. DOMAIN 118 127 COMPLEMENTARITY-DETERMINING 3. DOMAIN 128 138 FRAMEWORK 4. DISULED 41 115 BY SIMILARITY. NON TER 138 AA; 15576 MM; 110303 CN; DEQUENCE 138 AA; 15576 MM; 110303 CN; DOMAIN 128 138 SEQUENCE 138 AA; 15576 MM; 110303 CN; DOMAIN 128 138 AA; 15576 MM; 110303 CN; DOMAIN 128 138 AA; 15576 MM; 110103 CN; DOMAIN 138 AA; 15576 MM; 110103 CN; AACHA CONSERVAÇORILVIVA 135 DOMAIN 138 AA; 15576 MM; 11010 AA. BOMAIN 138 AA. BOM	FI	21 49 FRAMEWORF
DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.	FI	50 54 COMPLEMENTARIII-DELEKGINING 55 68 FRAMEWORK 2.
DOMAIN 118 127 COMPLEMENTARITY-DETERMINING 3.	FT	69 85 COMPLEMENTARITY-DETERMINING 86 117 FRAMEWORK 3.
DUMAIN 128 138 FTANEWORK 4. DISULER 138 A1 115 BY SIMILARITY. NON TERR 138 138 138 SEQUENCE 138 A2, 15576 MW; 110303 CN; SEQUENCE 138 A2, 15576 MW; 110303 CN; Duery Match 70.6%; Score 698; DB 4; Length 138; Sest Local Similarity 68.1%; Pred. No. 1.60e-129; Aatches 94; Conservative 25; Mismatches 16; Indels 3; Gap 1 11 11 11 11 11 11 11	F	118 127 COMPLEMENTARITY-DETERMINING
NON_TER 138 138 SEQUENCE 138 AA; 15576 MM; 110303 CN; Duery Match 70.6%; Score 698; DB 4; Length 138; Sest Local Similarity 68.1%; Pred. No. 1.60e-129; Astches 94; Conservative 25; Mismatches 16; Indels 3; Gap 11111 11111	FT	41 115
Duery Match 70.6%; Score 698; DB 4; Length 138; Sest Local Similarity 68.1%; Pred. No. 1.60e-129; Matches 94; Conservative 25; Mismatches 16; Indels 3; Gap 1 mgwsyiilfluvatatdvhsquqlqqqaelvkpqasvqlsckasqhtftnywihwvkqrp 1 mgwsyiilfluvatatdvhsquqlqqqaelvkpqasvqlsckasqhtftnywihwvkqrp 1 mGwSGIFLFLIS:::: : : : : : : : :	E 8	138 138 138 AA; 15576 MW;
mgwsyiilfluatatduhsquqlqqpaelukpgasvqlsckasghtftnywihwvkqrp	ÖMŽ	Match 70.6%; Score 698; DB 4; Length 138; Local Similarity 68.1%; Pred. No. 1.60e-129; es 94; Conservative 25; Mismatches 16; Indels
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61 ggglewigeinpndgrsnynekfknkatltvdkssstaymglssltpeefavyycarsdg :	Qy	: :: : :: :
	qq	ggglewigeinpndgrsnynekfknkatltvdkssstaymqlssltpeefavyycarsdg
121 yydwfvywggglutfsa 138 ::	Qy	
120NFAYWGGTLVTVSA 135 ULT 7 HV51 MOUSE STANDARD; PRT; 118 P06330; 01.1M 1988 (REL. 06, CREATED)	qq	
HU51 MOUSE STANDARD; PRT; 118 P06330; PLAN-1988 (REL. 06, CREATED)	θŷ	NRFAYWGQGTLVTVSA
P06330; 01-JAN-1988 (REL. 06,	RES!	7 V51_MOUSE STANDARD; PRT; 118
C	D T	1988 (REL. 06,

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1 evglqqsgpelvkpgasvkmsckasgytftdyymkwvkqshgkslewigdinpnnggtsy 60 20 EIQLQQSGPELAKPGASVKISCKASGYSFTSYYIHWVKQSHGKSLEWIGYIDPFNGGTSY 79 Gaps SCHILLING J., CLEVINGER B., DAVIE J.M., HOOD L.;
NATURE 283:35-40(1980).
-!- THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO BIND DEXTRAN
DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF WHICH OCCUR IN IG HEAVY CHAIN V REGION (VH558 A1/A4). ; MUS MUSCULUS (MOUSE). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; 68.3%; Score 675; DB 4; Length 117; 81.2%; Pred. No. 3.01e-124; Indels 10; Mismatches 11; 01-JAN-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
1G HEAVY CHAIN PRECURSOR V REGION (VH558 A1/A4).
MUS MUSCULUS (MOUSE). 21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN V REGION (J558). 117 AA 117 AA BY SIMILARITY 117 AA; 13024 MW; 82647 CN; PRT; HSSP, P01772, 1FOR.
IMMUNOGLOBULIN V REGION; SIGNAL.
SIGNAL 1 19 1G 1
CHAIN 20 117 IG 1 -!- THIS PROTEIN BINDS DEXTRAN. PIR; A26242; MHMSJ5. HSSP; P01789; 2FGW. IMMUNGLOBULIN V REGION. YANCOPOULOS G.D., ALT F.W.; CELL 40:271-281(1985). 95; Conservative THE D AND J SEGMENTS STANDARD; STANDARD; EMBL; M13787; MMIGHVA. PIR; A02029; HVMSAI. Best Local Similarity EUTHERIA; RODENTIA. EUTHERIA; RODENTIA SEQUENCE FROM N.A. LT 10 HV52_MOUSE P06327;

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RESULT

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FRAMEMORK 1. COMPLEMENTARITY-DETERMINING 1. FRAMEMORK 2. FRAMEMORK 2. FRAMEMORK 3. BY SIMILARITY. My; 71250 CN; Score 675; DB 4; Length 117; Score 675; DB 4; Length 117; 17. Misnather 31; Thele 0: Gang 0;	Jpelvkpgalvkisckasgytftsydinwvkc :	ggglewigwiypgdgstkynekfkgkatltadkssstaymglssltsensavyfcar 117 : : : :	### PRT; 117 AA. 101-2AA-1988 (REL. 06, CREATED) 101-2AA-1988 (REL. 06, LAST SEQUENCE UPDATE) 101-3AA-1988 (REL. 06, LAST SEQUENCE UPDATE) 101-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE) EUKRANOTA; MAJORANIA. EUKARNOTA; MAJORANIA. EUKARNOTA; MAJORANIA. 5509340 FERMENORUE FROM N.A. 5509340 FRANCOPOULOS G.D., ALT F.W.; FERLA 13788; MAJCHAB. PIR; A02035; MHASB4. 19 FRANENORK 1. DOMAIN RECION; SIGNAL. HAMINOGLOBULIN V RECION; VH558 B4). DOMAIN SO 49 FRANENORK 2. DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1. DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 2. DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2. DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2. DOMAIN 86 117 FRAMEMORK 2. DOMAIN 86 117 FRAMEMORK 3. DOMAIN 86 117 FRAMEMORK 3. DOMAIN 117 117 FRAMEMORK 3. DOMAIN 86 117 FRAMEMORK 3. DOMAIN 117 117 FRAMEMORK 3. DOMAIN 117 117 FRAMEMORK 3. DOMAIN 117 117 FRAMEMORK 3. DOMAIN 86 118 MISMATCHES 11; Indels 0; Gaps ches 88; Conservative 18; Mismatches 11; Indels 0; Gaps ches 88; Conservative 18; Mismatches 11; Indels 0; Gaps ches 88; Conservative 18; Mismatches 11; Indels 0; Gaps ches 88; Conservative 18; Mismatches 11; Indels 0; Gaps 11; Ill	KFKGKATLIVDKSSSTAIMHLSSLISEDSAVIICAR 11/
20 49 50 54 69 85 69 85 41 115 117 117 117 AA; 12971 MW; 68.3%; Sc milarity 78.6%; Pr	flfllsgtagvhcqvv : FLFLLSGTAGVHSEI	igwiypgdgstkyne : : : GYIDPFNGGTSYNQI	### HV49 MOUSE STANDAED; ### P06328; ### P	41GI LUPFINGGIS INQ
DOMAIN 20 DOMAIN 50 DOMAIN 55 DOMAIN 69 DOMAIN 86 DOMAIN 86 DISULFID 41 NON TER 117 SEQUENCE 117 AA; Query Match Marches 92: Conses		61 ggglew : 61 GKSLEW	HV49- P063Z D1-JA D1-JA D1-JA D1-NO D1-NO D1-NO D1-NO D1-NO D1-NO D1-NO D1-NO EUTHE EUTHE EUTHE EWBL; PIR; HSSP; HSSP; HSSP; HSSP; HSSP; HSSP; HSSP; HSSP; DOWAI DOWAI DOWAI DOWAI DOWAI DISUL DOWAI DISUL D	61 GKSLEV
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	RN [1]	SEQÜENCE 117 AA; Query Match Best Local Similarity Matches 88; Conser 1 mgwscilflvaaa
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ö Gaps grglewigridpnsggtkynekfkskatltvdtssstaymqlhsltsedsavyycar 117 ö Indels 17; Mismatches 12; Conservative 88; Jul 8 08:19

ö Gaps BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY -!- THIS GERMINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES. ; 0 EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; IG HEAVY CHAIN V REGION (145). COMPLEMENTARITY-DETERMINING 2. FRAMEWORK 3. Score 651; DB 4; Length 117; Pred. No. 9.34e-119; 18; Mismatches 12; Indels FRAMEWORK 1. COMPLEMENTARITY-DETERMINING 65.8%; 87; Conservative Best Local Similarity Query Match

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Best Local Similarity

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm

MPsrch pp

Mon Jul 8 08:30:57 1996; MasPar time 4.67 Seconds 239.615 Million cell updates/sec

Tabular output not generated.

Run on:

>US-08-137-117B-27 (1-135) from USO8137117B.pep 989 Title:

1 MGWSGIFLFLLSGTAGVHSE......ARGGNRFAYWGQGTLVTVSA 135 Description: Perfect Score:

PAM 150 -Gap 11 Scoring table:

Sequence:

70887 seqs, 8282111 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

a-geneseq22 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 Database:

Mean 29.935; Variance 137.631; scale 0.218 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	-78	-62	-61	09-	09-	09-	-59	-58	-58	-58	9-58	5-57
Pred. No	1.27e	3,43e	3.48e		•	~			~	~		٠.
Description	p12-h2.	81C6 heavy chain vari	KM-750 heavy chain.	KM-796 heavy chain.	puc-Rvh-1220d.	puc-Rvh-1220b.	Heavy chain variable	Heavy chain variable	Humanised anti-Tac an	Anti-Tac heavy chain	Mouse MAb 2G12 H chai	Heavy chain variable
ΩI	R28669	R62445	R53330	R53328	R29017	R29016	R05090	R12356	R24107	R06369	R12234	R08346
DB	و	12	10	10	9	9	 1	7	7	7	2	7
wery Aatch Length DB	135	137	137	139	135	135	137	141	135	135	140	144
Query	7.66	81.6	80.5	79.9	79.5	79.3	78.9	77.1	77.0	76.7	76.7	76.6
Score	986	807	196	790	786	784	780	763	762	759	759	758
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DREG-200 Ab heavy cha	Mouse C4G1 Ig heavy-c	Co-1 Heavy Chain V Re	Variable region of mu	Sequence encoded by a	encoded	Chimeric 128.1 VH, mo	7	Murine 128.1 VH/human	Ξ.	Cimeric antibody comp	Sequence of the heavy	Monoclonal antibody M	MAb SCH94.03 heavy ch	Murine anti-ICAM mono	R6-5-D6 anti-ICAM-1 h	Heavy chain variable	Mouse MAb 4D12 H chai	Anti-Leu 3a heavy cha	CIMO1 VH.	Sequence of murine an	p64-h2 protein produc	VH group	Murine monoclonal 14.	Mouse MAb 2E12 H chai	Heavy chain variable	Sequence of the heavy	Colon Cancer monoclon	Sequence of murine an	ME4 Heavy Chain V Reg	onal antiboc	on Cancer mo	VH425 antibody cloned
R55554	R39266	R09425	R06250	P70624	P93151	R38259	R41710	R41707	R41715	R41682	R59512	R40384	R84554	R15060	R15200	R12360	R12238	R04133	R33950	R38311	R29009	R21271	R11597	R12233	R12355	R59510	R04383	R38312	R09427	R13061	43	R27049
ន	œ	2	-	7	-	~	1	_	7	-	10	œ	14	m	٣	7	7	-	-	_	9	4	7	7	7	10	-	7	2	က	-	2
140	138	140	134	136	135	139	233	235	235	235	136	469	143	163	163	137	137	136	139	134	139	114	153	143	144	136	134	134	141	468	136	140
75.3	δ.	74.8	4	74.7	74.1	73.9	73.9	73.9	73.9	73.9	73.4	73.4	72.8	72.8	72.8	72.7	72.7	72.5	72.0	71.5	70.8	70.7	70.7	70.4	70.4		69.5	69.3			69.1	0.69
745	742	740	739	739	733	731	731	731	731	731	726	726	720	720	720	719	719	717	712	707	700	669	669	969	969	693	687	685	684	684	683	682
13	14	15	16	11	18	19	70	21	22	23	24	52	56	27	78	53	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                            61 GKSLERIGYIDPENGGTSYNQKFKGKATLTVDKSSSTAYMHLSSLTSEDSAVYYCARGGN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ggglewigyinpfndgtkynenfkgkatltsdrssstaymelssltseesavyfcardmg 120
                                                                                                                                                                                                                                                                                                                          gkslewigyidpfnggtsynqkfkgkatltvdkssstaymhlssltsedsavyycarggn 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 mewswiflfllsgtagvhsevqlqqsgpelvkpgasvkmsckasgytftsyvvhwvkqnp 60
                                                                        regions which were derived from a mouse monoclonal antibody produced from the hybridoma AUK12-20 which contained the plasmids p12-k2 and
                                                                                                                                                                                                                                               1 mgwsgiflfllsgtagvhseiqlqqsgpqlmkpgasvkisckasgysftsyyihwvkqsh 60
                                                                                                                                                                                                                                                                                   1 MGWSGIFLFLLSGTAGVHSEIQLQQSGPELMKPGASVKISCKASGYSFTSYYIHWVKQSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence is that of the monoclonal antibody 81C6 heavy chain variable region. The MAb may be administered to the cyst cavity of a human to treat cystic brain tumour, anaplastic astrocytoma and cystic glioblastoma and also solid tumours of the brain, kidney, spleen, prostate, breast, melonoma, or Wilms tumour.
                                     antibody which recognises human interleukin-6 receptor (IL-6R). The
                                                                                                                                                                                                          0; Gaps
The sequences given in R28668-69 were encoded by plasmid sequences
                                                                                                                                                                                                                                                                   coupled to therapeutic agent and admin. to the cyst cavity, also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for solid tumours after creation of an enclosed resection cavity
                                                        antibody comprises light (L) chain and heavy (H) chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treating cystic brain tumour with tenascin specific antibody
                   which were used in example to illustrate the production of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 807; DB 12; Length 137; Pred. No. 3.43e-62;
                                                                                                                                                                   Score 986; DB 6; Length 135; Pred. No. 1.27e-78;
                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tenacin; cyst; cystic brain tumour; astrocytoma; cystic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glioblastoma; Wilms tumour; cancer; breast; prostate.
                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 2A; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81C6 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R62445 standard; Protein; 137 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.6%;
80.3%;
                                                                                                                                                                   Query Match 99.7%;
Best Local Similarity 99.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 110; Conservative
                                                                                                                                                                                                          134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    121 rfaywgggtlvtvsa 135
                                                                                                                                                                                                                                                                                                                                                                                                                                          121 RFAYWGQGTLVTVSA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-MAR-1993; US-033827.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zalutsky M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAR-1994; U02703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 94-316668/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 AA;
                                                                                                                                 135 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             See also R62446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; Q73405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09421293-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-SEP-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bigner DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R62445;
                                                                                                              p12-h2.
                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
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5; 61 GKSLEWIGYIDPFNGGTSYNQKFKGKATLIVDKSSSTAYMHLSSLTSEDSAVYYCARGGN 120 1 mgwswiflfllsgtagvlsevqlqqsgpelvkpgasvkisckasgytftdynmdwvkqsh 60 vector for use in animal cells which contains the human Ab heavy and Gaps are introduced into animal cells and the transformant thus obtained is cultured for the prodn. of a chimeric human Ab reacting with the ganglioside GM2. In contrast to mouse monoclonal Abs, the chimeric human Abs will not cause anti-mouse Ig Ab prodn. in the patient's body but show a prolonged blood half-life, with a reduced frequency light chain constant region-encoding cDNA. The expression vectors of adverse effects, so that it can be expected to be superior to mouse monoclonal Abs in the efficacy in the treatment of human Chimeric human Ab expression vectors are constructed by inserting reacting with the ganglioside GM2 respectively into an expression isolated from hybridomas producing a mouse or rat monoclonal Ab 2; Mouse anti-GM2 monoclonal Ab KM-796 and KM-750 and rat KM-603 Score 796; DB 10; Length 137; Pred. No. 3.48e-61; the Ab heavy and light chain variable region-encoding cDNA chimeric antibody; expression vector; heavy; light; chain; Humanised antibody specific for ganglioside GM2 - used for Indels producing a cytocidal effect on cancers such as melanoma, CDR regions for use in chimeric Abs are indicated in the Nakamura K; hypervariable region; CDR; constant region; hybridoma; Ig; immunoglobulin; KM-796; KM-750; KM-603; cancer. heavy and light chain sequences are given in 045426-30 Monoclonal antibody; Ab; ganglioside GM2; chimera; 8; Mismatches 12; Kuwana Y, Disclosure; Page 107-108; 191pp; English. Location/Qualifiers JT 3 R53330 standard; Protein; 137 AA. Hanai N, Hasegawa M, Koike M, (KYOW) KYOWA HAKKO KOGYO KK. Query Match 80.5%; Best Local Similarity 83.9%; regfaywgqgtlvtvsa 137 17-NOV-1994 (first entry) 115; Conservative neuroblastoma and qlioma. 118..126 07-SEP-1992; JP-238452. 50..54 74..85 1..19 cancer, for instance. 07-SEP-1993; 046181. Peptide /label= sig_peptide KM-750 heavy chain. WPI; 94-126857/16. 137 AA; N-PSDB; Q45428 Features Table Mus musculus. /label= CDR1 /label= CDR2 /label= CDR3 AU9346181-A 17-MAR-1994 Shitara K; Sequence Region Region Region Matches 121 g 쉱 δ S

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Ou Be Ma	Query Match 79.9%; Score 790; DB 10; Length 139; Best Local Similarity 84.2%; Pred. No. 1.23e-60; Matches 117; Conservative 6; Mismatches 12; Indels 4; Gaps 2;
q	1 mgwswiflfllsgtagylsevglqgsgpelvkpgasvkisckasgytftdynmdwvkqsh 60
Qy	1 MGMSGIFLFLLSGTAGVHSEIQLQQSGPELMKPGASVKISCKASGYSFTSYYIHWVKQSH 60
Op	gkslewigyiypnnggtgynqkfkskatltvdkssstaymelhsltsedsavyycatygh
δò	61 GKSLEMIGYIDPFNGGTSYNQKFKGKATLTVDKSSSTAYMHLSSLTSEDSAVYYCAR-G- 118
q 0	121 yygymfaywgggtlvtvsa 139
ζŷ	119GNRFAYWGQCTLVTVSA 135
RESULT	75
N P	R29017; R29017;
TO	30-MAR-1993 (first entry)
ž	interleukin-6; receptor; IL-6R; CDR; PCR;
¥ ¥	complementarity determining region; monoclonal; hybridoma; PCR; nlagmid: nolymerase chain reaction; amplify.
08	thetic.
FH	Key Location/Qualifiers
FT	Leader r
FT	i
H	/label= FRI
FI	Abel= CDR1
FI	
FF	/label= FR2
. H	Abbel= CDR2
FT	
F	- FR3
1.5	Region 118124 Jaba
. E.	
FT	/label= FR4
N. C	W09219759-A.
먑	12-NOV-1992; 24-APR-1992; J00544.
PR	25-APR-1991; JP-095476.
E E	19-FEB-1992; JP-032084.
P.A.	(CHUS) CHUGAI SEITAKU KK. Dondin MW Inno ST Sildaha Ta Sato K Touchius W.
DR E	im, vones bi, baldanna om, baco 6, isuchiya -398882/48.
DR	N-PSDB; Q31391.
E E	Reconstituted human antibody to human interleukin-6 receptor -
7 5	nas Iow ancigenicity and contains mouse V-Tegion complementailly determining regions
PS	Disclosure; Page 159-60; 207pp; Japanese.
႘	The sequences given in R29016-17 are portions of monoclonal antibodies
ဗ ဗ	which were encoded by plasmids contained within the mouse hybridoma, MIR12_20 The DNA encoding the complementarity determining regions
88	(CDR's) was isolated by polymerase chain reaction. These antibodies
ខ	se human interleukin-6 receptor (IL-6R). The hybri

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(CDR's) was isolated by polymerase chain reaction. These antibodies recognise human interleukin-6 receptor (IL-6R). The hybridoma cells were transformed with plasmids containing fragments of the antibody gene which caused the production of the antibody from the hybridoma

5 Gaps 5; Query Match 79.3%; Score 784; DB 6; Length 135; Best Local Similarity 75.0%; Pred. No. 4.35e-60; 20; Mismatches 12; Indels 102; Conservative

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60 pggglewvgyidpfnggtsyngkfkgkvtmtvdtstntaymelsslrsedtavyycargg 119

60 HGKSLEMIGYIDPFNGGTSYNQKFKGKATLIYUDKSSSTAYMHLSSLTSEDSAVYYCARGG 119

120 nrfaywgqgtlvtvss 135

R05090 standard; protein; 137 AA. (first entry) 10-MAR-1993 (revised) 04-0CT-1990 (first en

Heavy chain variable domain of human chorion gonadotrophin-binding pptde. Human chorionic gonadotropin; antibodies; heavy chain; choriocarcinoma; abortion; tumour detection; complementary determining regions;

Location/Qualifiers 50..54

118..126 70..85

WPI; 90-165307/22. van Wezenbeek PM;

Polypeptide(s) which specifically bind human chorionic gonadotropin contg. antigen-binding domains comprising complementary

determining domains.

Disclosure; p; English. Togheter with the light chain variable domain (R05089) the sequence forms a hCH-binding antibody fragment (FhCG). For the production of Abs fragment (FhCG). For the production of Abs the variable region was fused to a constant region of human origin.

diagnosis, eg for localisation of tumours and for in vitro diagnosis for detection of hCG in body fluids. 137 AA;

78.9%; Score 780; DB 1; Length 137;

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RESULT 쇰 ð 쇰 3 임 δ :: ä 61 gqslewigginpnnggttynqkfkdkatlivdkssstaymdvrsltsddsavyycarrgn 120 61 GKSLEWIGYIDPFWGGTSYNQKFKGKATLTVDKSSSTAYMHLSSLTSEDSAVYYCAR-G- 118 61 grslewigyjypysgptgyngrfnskatltvdnssstafmevrsltsedsavyycaregi 120 61 GKSLEMIGYIDPFNGGTSYNQKFKGKATLTVDKSSSTAYMHLSSLTSEDSAVYYCARGGN 120 1 mgwswiflfllsgtagvlsevqlqqsgpelvkpgasvkiscktsgytfteytihwvkqsh 60 1 MGWSGIFLFLLSGTAGVHSEIQLQQSGPELMKPGASVKISCKASGYSFTSYYIHWVKQSH 60 mgwswiflfllsgtagvhsevqlqqsgpelvkpgasvkisckasgytftdynmhwvkqsh 60 1 MGWSGIFLFLLSGTAGVHSEIQLQQSGPELMKPGASVKISCKASGYSFTSYYIHWVKQSH 60 6; Gaps 2; Gaps light chain V-regions are joined by manipulating their respective joining (J) regions, to generate restriction enzyme recognition sites. The chimeric Mabs can be used as immunoconjugates, in association with e.g. toxins for HIV treatment. They can also be used in diagnosis of HIV. This is the heavy-chain variable (V) region of a mouse monoclonal antibody (MAb), 2G12, and is specific for an HIV-1 viral antigen. It is used in the construction of a chimeric MAb comprising heavy The chimeric MAbs are more effective than murine MAb 2G12 since they have an increased compatibility in humans. The heavy and New chimeric mouse-human antibodies - used to detect, kill and and light chains having murine V regions and human C regions. Score 763; DB 2; Length 141; Pred. No. 3.61e-58; 9; Mismatches 12; Indels Heavy chain variable region of murine 2G12 immunoglobulin. 17; Mismatches 11; Indels Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR; WPI; 91-178044/24. Chimeric antibodies; immunoconjugates; HIV; AIDS Best Local Similarity 78.1%; Pred. No. 1.01e-59; Disclosure; fig 7; 107pp; English. See also <u>012</u>056-57 and <u>012059-63.</u> R12356 standard; Protein; 141 AA. remove HIV-1 antigen from sample || :|||||| ||||||| 119 ---GN-RFAYWGQGTLVTVSA 135 121 lyygnfwfaywgqgplvtvsa 141 77.1%; 80.9%; 121 fytmdywgqgtsvtvss 137 121 RFA--YWGQGTLVTVSA 135 15-AUG-1991 (first entry) 107; Conservative 114; Conservative 30-MAY-1991. 13-NOV-1990; U06615. 13-NOV-1989; US-433730. (XOMA-) XOMA CORP. (GREC) GREEN CROSS CORP = = = = Best Local Similarity 141 AA; N-PSDB; Q12058. Mus musculus. WO9107493-A. 30-MAY-1991 Query Match Sequence Matches Matches a ð 셤 음 ð g à 유 쇰 ð δ δ

replaced with the corresponding amino acids in the anti-Tac heavy chain antibody. This produces a humanised antibody which has the same affinity as anti-Tac for IL-2 receptors. The Ig may be used to treat humans with T-cell related diseases such as transplant rejection, T cell leukaemia, or autoimmune diseases such as diabetes or multiple sclerosis. See also R24103-R24108. 61 gqglewigyinpstgyteynqkfkdkatitadestntaymelsslrsedtavyycarggg 120 61 GKSLEWIGYIDPFWGGTSYWQKFKGKATLTVDKSSSTAYMHLSSLTSEDSAVYYCARGGN 120 that reacts specifically with p55-Tac protein and/or inhibits binding of human interleukin-2 (IL-2) to its specific receptor. The three complementarity determining regions and amino acids 27, 30, 48, 67, 68, 93, 95, 98, 107, 108, 109 and 111 of human antibody Eu have been 1 mgwswiflfllsgtagvhsgvqlvqsgaevkkpgssvkvsckasgytftsytmhwvrqap 60 Gaps Disclosure; Fig 3; 21pp; German. The sequence is that of the humanised anti-Tac antibody heavy chain which is used in the production of a human-type immunoglobulin (Ig) New humanised antibody specific for interleukin-2 receptor - with Immunoglobulin; T cell related diseases; leukaemia; autoimmune; complementarity determn. regions and framework from different immunoglobulin(s), is non immunogenic and used to treat T-cell ö 77.0%; Score 762; DB 2; Length 135; Pred. No. 4.46e-58; 18; Mismatches 17; Indels IL-2 receptor; recombinant; diagnosis; therapy Humanised anti-Tac antibody heavy chain. Anti-Tac heavy chain variable region. Location/Qualifiers LT 10 R06369 standard; protein; 135 AA. R24107 standard; Protein; 135 AA. (PROT-) PROTEIN DESIGN LABS INC. Best Local Similarity 74.1%; 100; Conservative R06369; 13-DEC-1990 (first entry) (first entry) 121 vfdywgggtlvtvss 135 "signal peptide" 20..135 17-JAN-1990; DD-337159. "mature peptide" 17-JAN-1990; 337159. Queen CL, Selick HE. WPI; 92-167794/21. mediated disorders N-PSDB; Q24790. 25-NOV-1992 DD-296964-A. 19-DEC-1991. Synthetic. Query Match Peptide Peptide R24107; /note= Matches

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ñ 61 GKSLEWIGYIDPFNGGTSYNQKFKGKATLTVDKSSSTAYMHISSLTSEDSAVYYCAR-G- 118 61 gqslewigginpnnggttynqkfkdkatlivdkssstaymdvrsltsddsavyycarrgn 120 The MAD recognises the epitope on alpha/beta TCR and includes a mediator resonse. It is highly effective in clinical application before, after and during bone marrow transplant surgery, in treatment of cancer and autoimmune diseases, and has applications in 1 mgwswiflfllsgtagvlsevqlqqsgpelvkpgasvkiscktsgytfteytihwvkqsh 60 6; Gaps New chimeric mouse human antibodies – used in treatment, diagnosis and prophylaxis of HIV infections. Disclosure; Fig 7; 108pp; English. treatment, diagnosis and prophylaxis of HIV infections, and may be Human alpha/beta T-cell receptor; TCR; cancer; autoimmune disease. The mouse VH gene product may be used to produce chimeric mouse-human Abs against HIV-1 comprising human Ig constant regions and produced by a bacterial, yeast or mammalian expression system. therapeutic agent for immuno-regulation, e.g. to treat cancer Disclosure; Table 1A; 44pp; English. used for immunosuppressive therapy in transplantation and in N-PSDB; Q06955, Q06957. Anti-human alpha-beta T-cell receptor monoclonal antibodies murine variable regions. These novel sequence are useful in Query Match 76.7%; Score 759; DB 2; Length 140; Best Local Similarity 80.7%; Pred. No. 8.38e-58; 9; Mismatches 12; Indels Heavy chain variable region of the BMA-031 MAb. Kurrie R, Shearman CW, Moore GP, Seiler F; Location/Qualifiers .T 12 R08346 standard; protein; 144 AA. 121 lyygnfwfaywgggplvtvs 140 || :||||||| |||||| 119 ---GN-RFAYWGQGTLVTVS 134 05-MAR-1991 (first entry) 113; Conservative 118..128 (BEHW) BEHRINGWERKE AG. 07-JUN-1989; US-362549. 25-MAY-1990; US-529979. 69..85 (GENZ-) GENZYME CORP 19-DEC-1990. 07-JUN-1990; 306178. WPI; 91-178106/24. 140 AA

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9 61 ggglewigyinpyndvtkynekfkgkatltsdksssraymelssltsedsavhycargsy 120 61 GKSLEMIGYIDPENGGTSYNQKFKGKATLTVDKSSSTAYMHLSSLTSEDSAVYYCARGG- 119 4; Gaps 1 mewswiflfllsgtagvhsevqlqqsgpelvkpgasvkmsckasgykftsyvmhwvkqkp 60 1 MGWSGIFLFLLSGTAGVHSEIQLQQSGPELMKPGASVKISCKASGYSFTSYYIHWVKQSH 60 chain variable region frameworks of the human acceptor antibody Eu. Nucleotide and as sequences are provided for the DREG-200 light (Q66699, R5553) and heavy (Q66700, R5554) chain variable regions and the humanized DREG-200 light (Q66701, R55555) and heavy (Q66702, R55556) chain variable regions. The humanized antibodies can be produced economically in large quantities by expression in mammalian DREG-200 Ab heavy chain variable region.

DREG-201; L-selectin; LECAM-1; Mel-14; IAM-1;
humanized antibody; immunoglobulin; Ig; IgG1; IgG4;
complementarity determining region; CDR; monoclonal antibody; MAb;
framework; light chain; heavy chain; variable domain;
monoclonal antibody; acceptor antibody Eu; transgenic animal. New humanised antibody specific for L-selectin - with murine CDR and human framework regions, inhibits binding of neutrophils to endothelial cells and useful for treating or preventing corresponding to those of mouse MAb DREG-200 and heavy and light An L-selectin-specific IgG1 or IgG4 humanized antibody has CDRs Abs may also be used in detection of immunocompetent T-cells Score 758; DB 2; Length 144; Pred. No. 1.03e-57; 10; Mismatches 16; Indels US-08-137-117B-27.rag cell culture or in transgenic animals. Location/Qualifiers Disclosure; Fig. 1B; 60pp; English. R55554 standard; Protein; 140 AA. 01-DEC-1992; US-983946. (PROT-) PROTEIN DESIGN LABS INC. 121 ydydgfvywgggtlvtvsa 139 120 -N-R-FAYWGQGTLVTVSA 135 76.6**%**; 78.4**%**; 16-NOV-1994 (first entry) 109; Conservative 118..129 50..54 69..85 ...19 'label= Sig peptide 30-NOV-1993; U11612. Best Local Similarity 94-199974/24. P-PSDB; Q66700. Region /label= CDR2 Region /label= CDR3 /label= CDR1 W09412215-A. 09-JUN-1994 Sequence Sequence Query Match Peptide Mus sp. Region Co MS; Matches DET THE FET THE PROPERTY OF THE PARTY OF THE ပ္တင္တ g g 쇰 ð à ð

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Claim 13, Page 123 + Fig 22; 173pp; English.

The sequence is used in the prodn. of a chimeric antibody mol. comprising two light chains and two heavy chains, each having a constant region (human) and a variable region (murine) having specificity to an antigen bound by murine monoclonal antibody (MAA) Co-1. The chimeric antibodies can be used for any purpose for which the original murine MAbs can be used for any purpose that
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Co-1 Heavy Chain V Region (mouse).
Monoclonal antibody; chimera; light; heavy; chain; constant; variable; antigen; diagnosis; cancer; tumour.
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Pred. No. 4.55e-56;
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N-PSDB; Q08607.
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R09425 standard; Protein; 140 AA.
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06-SEP-1989; U03852.

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08-SEP-1988; US-241744.

13-SEP-1988; US-243139.

04-OCT-1989; US-357641.

21-JUL-1989; US-367641.

21-JUL-1989; US-367641.
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

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protein - protein database search, using Smith-Waterman algorithm MPsrch pp

Mon Jul 8 08:32:11 1996; MasPar time 7.21 Seconds 445.389 Million cell updates/sec Run on:

Tabular output not generated.

Title:

>US-08-137-117B-29 (1-127) from USO8137117B.pep 909 Description: Perfect Score:

1 MVSSAQFLGLLLLCFQGTRC......CQQGNTLPYTFGGGTKLEIN 127 Sequence:

PAM 150 Gap 11 Scoring table:

82306 seqs, 25270970 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

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Mean 41.024; Variance 138.493; scale 0.296 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Pred. No.	2.52e-89	2.43e - 88	1.33e-87	6.50e-84	5.74e-81	1.63e-78	2.52e-70	1.80e-69	1.80e-69	2,38e-69	7.32e-69	9.70e-69
		Description	Iq kappa chain precu	Ig kappa chain V reg	kappa chain	Ig kappa chain precu	immunoglobulin kappa	Iq light chain precu	Ig kappa chain V reg	Ig kappa chain V reg	Ig kappa chain V reg	Iq kappa chain V req	chain	>
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(M-T151) - human (name man -Apr-1993 ftext_cha	uza, B.; Schwirzke, H.; Weiss, E.H.; Ri U.H.	imeric antibodies d o the alpha-chain o		ion; immunoglobulin	tus predicted #labe gion #status predic	
PH1224 #type fragment Ig kappa chain precursor V region (M-7151) - human (fragment). #formal name Homo sapiens #common_name man 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change	PH1224 PH1224 PH1224 Reissenbrn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reizer, C.; Elieger, D.; Lenz, H.; Weiss, E.H.; Rieber, E.P.; Riethmueller, G.; Weidle, U.H.	Gene (1992) 121:271-278 Combinatorial functions of two chimeric antibodies directed to human CD4 and one directed to the alpha-chain of the human interleukin-2 receptor.	4 mRNA 1-127 ##label WEI	fsuperfamily immunoglobulin V region; immunoglobulin homology immunoglobulin	<pre>#domain signal sequence #status predicted #label SIG\ *product Ig light chain V region #status predicted #label MAT</pre>	#length 127 #checksum 4396
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RESULT 1 ENTRY TITLE ORCANISM DATE	ACCESSIONS REFERENCE #authors	#journal #title	#accession ##molecule ##residues	CLASSIFICATION KEYWORDS FEATURE	1-20 21-127	SUMMARY

96.4%; Score 876; DB 5; Length 127;

Query Match

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#superfamily immunoglobulin V region; immunoglobulin homology
#length 128  #molecular-weight 14078  #checksum 4901
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J. Biol. Chem. (1990) 265:133-138
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Proc. Natl. Acad. Sci. U.S.A. (1987) 84:1085-1089
V-K and J-K gene segments of A/J Ars-A antibodies: somatic recombination generates the essential arginine at the junction of the variable and joining regions.
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Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.
J. Biol. Chem. (1987) 262:13579-13583
Nucleotide and translated amino acid sequences of CDNA coding
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#superfamily immunoglobulin V region; immunoglobulin homology
#length 126 #molecular-weight 13839 #checksum 3586
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31-Dec-1988 #sequence revision 31-Dec-1988 #text_change
Active site structure and antigen binding properties of
                                                                                                                                                                                                                                                                                                           Ig kappa chain precursor V region (AC-1001) - mouse
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product Ig light chain #status predicted #label MATV

fregion complementarity-determining 1/ fregion complementarity-determining 2

86.78;

domain signal sequence (fragment) #label

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Meek, K.; Sanz, I.; Rathbun, G.; Nisonoff, A.; Capra, J.D. Proc. Natl. Acad. Sci. U.S.A. (1987) 84:6244-6248 Identity of the V-kappa-10-Ars-A gene segments of the A/J and BALB/c strains.

12-Apr-1995 B28044

A94179

#cross-references MUID:87317629

FEATURE

##cross-references EMBL:X65095 Best Local Similarity 96.5%; 109; Conservative #description CLASSIFICATION submission ##status #accession Query Match œ authors ACCESSIONS REFERENCE authors ijournal Matches ACCESSIONS #title TITLE ORGANISM REFERENCE 7-115 30-40 56-62 ORGANISM SUMMARY SUMMARY RESULT RESULT ENTRY ENTRY DATE DATE В δ 임 ð 임 δ P P δ #superfamily immunoglobulin V region; immunoglobulin homology ö 98 Kaartinen, M.; Rocca-Serra, J.; Maekelae, O. Mol. Immunol. (1988) 25:859-865 Combinatorial association of V genes: one VH gene codes for specific for a different antigen (phoxazolone, NP or GAT) fcross-references MUID:89096973 the authors translated the codon AGG for residue 30 Kim, S.O.; Sanz, I.; Williams, C.; Capra, J.D.; Gottlieb, P.D. Gaps Ig light chain precursor V region (anti-phenyloxazolone, 18C10) - mouse (fragment) #formal name Mus musculus #common name house mouse 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 02-May-1994 #sequence_revision 18-Nov-1994 #text_change three non-cross-reactive monoclonal antibodies each Polymorphism in V kappa 10 genes encoding L chains of antibodies bearing the Ars-A and A48 cross-reactive ##cross-references NCBIN 62777; NCBIP:62780
##experimental_source AJI strain
##note sequence extracted from NCBI backbone

ry #length 115 #molecular-weight 12681 #checksum 7342 formal name Mus musculus #common name house mouse .**.** Score 808; DB 11; Length 115; Pred. No. 5.74e-81; 0; Indels immunoglobulin kappa variable chain - mouse Immunogenetics (1991) 34:231-241 4; Mismatches #type fragment #type complete 1-115 ##label KAA 1-115 ##label KIM cross-references MUID: 92010099 preliminary Query Match 88.9%; Best Local Similarity 96.5%; Matches 111; Conservative 28-Apr-1995 A53276 A53276 12-Apr-1995 JL0080 idiotypes. ##molecule_type mRNA ##molecule_type DNA JL0080 A53276 JI0076 JL0080 ##residues ##residues CLASSIFICATION 127 N 127 121 k 121 #status #accession #accession ##note #authors S #authors fjournal #journal ACCESS IONS ACCESSIONS #title #title REFERENCE REFERENCE ORGANISM ORGANISM SUMMARY RESULT RESULT TITLE LITLE ENTRY DATE

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#authors authors | journal Matches ACCESSIONS **ACCESSIONS** 81 TITLE ORGANISM 8 #title REFERENCE REFERENCE ORGANISM SUMMARY SUMMARY RESULT ENTRY DATE g 음 ð 염 δ S 염 ð #superfamily immunoglobulin V region; immunoglobulin homology flength 107 #molecular-weight 11738 #checksum 7011 #superfamily immunoglobulin V region; immunoglobulin homology Proc. Natl. Acad. Sci. U.S.A. (1981) 78:7679-7683 Complete amino acid sequence of light chain variable regions ö ö KVMSAR #type complete Ig kappa chain V regions (anti-arsonate hybridoma proteins) 1 digmtqttsslsaslgdrvaiscrasqdisnylnwyqqkpdgtvklliyytsrlhsgvps 60 21 DIQMIQITSSLSASLGDRVIISCRASQDISSYLAWYQQRDGTIKLLIYYTSRLHSGVPS 80 1 digmtqttsslsaslgdrvtiscrasqdisnylnwyqqkpdgtvklliyytsrlhsgvps 60 21 DIQMTQTTSSLSASLGDRVTISCRASQDISSYLMWYQQKPDGTIKLLIYYTSRLHSGVPS 80 Gaps Gaps #formal name Mus musculus #common name house mouse 06-Jul-1982 #sequence_revision 06-Jul-1982 #text_change derived from five monoclonal anti-p-azophenylarsonate antibodies differing with respect to a crossreactive #disulfide_bonds #status predicted #length 108 #molecular-weight 11910 #checksum 1537 ö ; 0 Length 107; 78.5%; Score 714; DB 2; Length 108; 94.4%; Pred. No. 1.80e-69; 1; Indels 1; Indels 81 RFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGGGTKLEIN 127 61 rfsgsgsgtdysltisnlegediatyfcgggntlprtfgggtkleik 107 61 rfsgsgsgtdysltisnleqediatyfcqqqnslprtfgggtkleik 107 Score 714; DB 5; Pred. No. 1.80e-69; 5; Mismatches 5; Mismatches Siegelman, M.; Capra, J.D. #cross-references MUID:82150934
#accession A01927 78.5%; 94.48; 101; Conservative 101; Conservative 05-Apr-1995 idiotype ##molecule_type_mRNA mouse Best Local Similarity Best Local Similarity ##residues CLASSIFICATION CLASSIFICATION Query Match Query Match σ **!**authors | journal Matches ACCESSIONS Matches title REFERENCE ORGANISM 23-88 SUMMARY SUMMARY TITLE

ENTRY

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Meek, K.; Sanz, I.; Rathbun, G.; Nisonoff, A.; Capra, J.D. Proc. Natl. Acad. Sci. U.S.A. (1987) 84:6244-6248 Identity of the V-kappa-10-Ars-A gene segments of the A/J and homology Production and cloning of TMV-specific monoclonal antibodies ö ; 21 DIQMIQTISSLSASLGDRVIISCRASQDISSYLAWYQQRPDGTIKLLIYYTSRLHSGVPS 80 1 digmtgttsslsaslgdrvtiscrasgdisnylnwyggkpdgtvklliyytsrlhsgvps 60 1 dvqmtqttsslaaslgdrvtiscrasqdisnylnwyqqkpdgtvklliyytsrlhsgvps 60 Gaps #formal name Mus musculus #common name house mouse 19-May-1989 #sequence_revision 19-May-1989 #text_change 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change #superfamily immunoglobulin V region; immunoglobulin flength 107 #molecular-weight 11832 #checksum 7241 Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F. #length 108 #molecular-weight 11865 #checksum 1422 Ig kappa chain V region - mouse #formal name Mus musculus #common name house mouse ; 0 1; Indels 1; submitted to the EMBL Data Library, August 1993 Length 108; Query Match 78.4%; Score 713; DB 5; Length 107; Best Local Similarity 94.4%; Pred. No. 2.38e-69; 61 rfsgsgsgtdysltisnleqediatyfcqqgntlppwtfgggtkleik 108 2; Indels 61 rísgsgygtdysltinnleqediatyfcqqgktlprtfgggtkleik 107 kappa chain V region (22B5) - mouse Score 709; DB 11; Pred. No. 7.32e-69; 6; Mismatches 4; Mismatches #type complete ##molecule_type mRNA ##residues 1-107 ##label MEE 1-108 ##label FIS ##cross-references EMBL:X75854 #cross-references MUID:87317629 BALB/c strains. preliminary Query Match 78.0%; Best Local Similarity 92.6%; Matches 100; Conservative 101; Conservative 06-Feb-1995 ##molecule_type mRNA A28044 A94179 538862 S38862 A28044 538862 537200 ##residues description CLASSIFICATION submission ##status #accession #accession 12 RESULT ENTRY

#type fragment

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#type complete

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RESULT ENTRY

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#superfamily immunoglobulin V region; immunoglobulin homology #superfamily immunoglobulin V region; immunoglobulin homology ö genes expressed by independently generated hybridomas apparently acquired by point mutation and selection rather ö variable regions from two λ/J mouse antigen nonbinding monoclonal antibodies bearing the predominant p-azophenyl Biochemistry (1987) 26:604-612 Complete amino acid sequences of the heavy and light chain by somatic processes: Consecutive shared somatic alterations in VH #type fragment chain V region (45-49, anti p-azophenylarsonate) 1 digmtqttsslaaslgdrvtiscrasqdisnylnwyqqkpdqtvklliyytsklksgvps 60 21 DIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKPDGTIKLLIYYTSRLHSGVPS 80 Gaps Gaps B26405 #type complete
Ig kappa chain V region (1F6) - mouse
#formal_name Mus musculus #common_name house mouse
30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change #formal_name Mus musculus #common_name house mouse 24_Feb-1994 #text_change #length 108 #molecular-weight 11985 #checksum 1541 ö ö Wysocki, L.J.; Gefter, M.L.; Margolies, M.N. J. Exp. Med. (1990) 172:315-323 Parallel evolution of antibody variable regions Length 108; Length 108 Indels 61 rfsgsgsgtdysltisdlehediatyfcqqgntlprtfgggtkleik 107 5; Query Match 76.7%; Score 697; DB 5; I Best Local Similarity 91.6%; Pred. No. 2.12e-67; Score 694; DB 5; 1 Pred. No. 4.91e-67; 7; Mismatches 5; Mismatches Smith, J.A.; Margolies, M.N. #length 108 #checksum 960 than by gene conversion antibody; immunoglobulin 1-108 ##label WYS 1-108 ##label SMI ##experimental source strain A/J ##experimental source A/J mice arsonate idiotype. \$\frac{1}{2}cross-references MUID:87157677 mouse (fragment) Query Match 76.3%; Best Local Similarity 92.5%; 98; Conservative 30-Sep-1993 99; Conservative 09-Sep-1995 #molecule_type protein ##molecule_type mRNA ig light B26405 A90518 PL0282 B26405 PL0281

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Search completed: Mon Jul 8 08:32:39 1996 Job time: 28 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch pp

Mon Jul 8 08:31:42 1996, MasPar time 4.05 Seconds 480.396 Million cell updates/sec Run on:

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Description: Perfect Score:

>US-08-137-117B-29 (1-127) from US08137117B.pep 909 1 MVSSAQFLGLLLLCFQGTRC.........CQQGNTLPYTFGGGTKLEIN 127 Sequence:

PAM 150 Gap 11 Scoring table:

43470 seqs, 15335248 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot31
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Mean 41.298; Variance 69.545; scale 0.594 Statistics:

SUMMARIES

1 714 78.5 108 4 KV5K MOUSE 2 711 78.2 108 4 KV5L MOUSE 3 710 78.1 108 4 KV5L MOUSE 5 698 76.8 108 4 KV5M MOUSE 6 684 75.2 108 4 KV5M MOUSE 7 653 71.8 108 4 KV5M MOUSE 8 627 69.0 129 4 KV1M HUMAN 9 618 68.0 129 4 KV1M HUMAN 11 593 65.2 117 4 KV1I HUMAN 11 593 65.2 117 4 KV1I HUMAN 12 551 65.0 128 4 KV1K HUMAN 13 551 65.0 128 4 KV1K HUMAN	Result No.	Score	Query Match	Query Match Length DB	DB	a a	Description	ion		Pred. No.
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A 901 0 63	12	591	65.0	128	4	KV5E_MOUSE	IG KAPPA	CHAIN	PRECUR	9.82e-112
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					_			EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;							PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).				DY.		COMPLEMENTARITY-DETERMINING 1		COMPLEMENTARITY-DETERMINING 2.		COMPLEMENTARITY-DETERMINING		
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	108 AA.			PDAT	UPE			AIA;							-168				AN	FRAMEWORK 1.	NTAF	FRAMEWORK 2.	NTAF	FRAMEWORK 3.	NTAF	FRAMEWORK 4.	BY SIMILARITY.
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	PRT;			E	JTAT	316.		VERT							78:7	CEL			RSON	RAME	MPI	RAME	PMPI	RAME	IdWO	RAME	Y S]
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			21-JUL-1986 (REL. 01, CREATED)	LAST SEQUENCE UPDATE)	01-oct-1993 (REL. 27, LAST ANNOTATION UPDATE)	IG KAPPA CHAIN V-V REGION (HP R16.7).		NAT.						-:	J.S.	-!- ANTI-ARSONATE HYBRIDOMA PROTEIN.			IMMUNOGLOBULIN V RECION; ANTIARSONATE ANTIBODY.								
	STANDARD;		៊	Ξ,	1	EGI		CHO						J.D	:	BRII			ION	23	34	49	99	88	16	108	88
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	S		ÆĽ.	(REL. 01,	REL,	'> N	MUS MUSCULUS (MOUSE).	TAZ	EUTHERIA; RODENTIA.					SIEGELMAN M., CAPRA J.D.;	CAD	NATE	PIR; A01927; KVMSAR.	HSSP; P01607; 1FAI.	N N	-	24	32	20	57	83	86	23
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	KV5K_MOUSE		-198	21-JUL-1986	-19	PA (SCUI	OTA	IA;		띥	STRAIN=A/J;	34	MAN	NAT	TI-1	019	P01	GIO								В
_	×ί	P01644;	Ė	Ę	-OCT	KAP	B	CARY	HER		SEQUENCE.	MIN	82150934	SGEL	č,	AN.	¥ ::	3P ;	ON O	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DISULFID
텀	Š	P01	21-	21-	1	ΣI	M	B	EG.	Ξ	贸	STF	82]	SIE	PR	÷:	PII	HS	Ħ	õ	Ö	ğ	õ	Õ	õ	8	D
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FRAMEWORK 2. COMPLEMENTARITY-DETERMINING LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE) FRAMEWORK 3. FRAMEWORK 4. FRAMEWORK 1. FRAMEWORK 2. MW; 63856 CN; 21-JUL-1986 (REL. 01, IAST SEQUENCE 01-OCT-1993 (REL. 27, LAST ANNOTATION IG KAPPA CHAIN V-V REGION (HP 124E1) 23 34 49 49 56 88 97 108 88 108 Best Local Similarity 93.5%; Matches 100; Conservative SIEGELMAN M., CAPRA J.D.; STANDARD; 23 34 49 56 MUS MUSCULUS (MOUSE). PIR; A01927; KVMSAR. EUTHERIA; RODENTIA. 108 AA; EUTHERIA; RODENTIA. HSSP; P01607; 1FAI HSSP; P01607; 1FAI STRAIN=A/J; 82150934 STRAIN=A/J; KVSM MOUSE SEQUENCE. DISULFID Query Match 82150934 SEQUENCE SEQUENCE P01646; DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN NON TER DOMAIN DOMAIN RESULT g g δ δ ö ö 21 DIQMIQITSSISASIGDRVIISCRASQDISSYLNWYQQRDGTIKLLIYYTSRLHSGVPS 80 1 digmtgttsslsaslgdrvtiscrasgdisnylnwyggkpdgtvklliyytsrlhsgvps 60 21 DIQMIQITSSLSASLGDRVIISCRASQDISSYLAWYQQRDGTIKLLIYYTSRLHSGVPS 80 1 digmtgttsslsaslgdrvtiscrasgdisnylnwyggkpdgtvklliyytsrlhsgvps 60 Gaps Gaps ., 0 MUS MUSCULUS (MOUSE). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; RODENTIA. ; COMPLEMENTARITY-DETERMINING 1. COMPLEMENTARITY-DETERMINING 2. COMPLEMENTARITY-DETERMINING 3. Score 714; DB 4; Length 108; Pred. No. 1.57e-141; Score 711; DB 4; Length 108 Pred. No. 8.46e-141; 5; Mismatches 1; Indels Indels 61 rfsgssgstdysltisnleqediatyfcqqgnmlprtfgggtkleik 107 ; PROC. NATL. ACAD. SCI. U.S.A. 78;7679-7683(1981). -!- ANTI-ARSONATE HYBRIDOMA PROTEIN. PIR; A01927; KVMSAR. HSSP; P01607; 1FAI. IMMUNOCLOBULIN V REGION; ANTIARSONATE ANTIBODY. DOMAIN 1 23 FRAMEWORK 1. 21-JUL-1986 (REL. 01, IAST SEQUENCE UPDATE) 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE) IG KAPPA CHAIN V-V REGION (HP 93G7), 108 AA. 4; Mismatches 108 AA BY SIMILARITY, FRAMEWORK 4. FRAMEWORK 2. FRAMEWORK 3. 11954 MW; 63046 CN; 11910 MW; 63325 CN; PRT; P01645; 21-JUL-1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 01, CREATED) 94.48; 78.2%; 94.4%; 78.5%; 101; Conservative 101; Conservative SIEGELMAN M., CAPRA J.D.; STANDARD; STANDARD; 23 34 56 56 97 108 108 108 1 108 AA; 24 35 50 57 89 98 23 108 Best Local Similarity Best Local Similarity

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SEQUENCE 82150934

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1 digmtqttsslsaslgdrvtiscrasqdinnylnwyqqkpdgtvklliyytsrlhsgvps 60 21 DIQMIQTISSLEASLEGRATISCRASQDISSYLNWYQQKPOGTIKLLIYYTSRLHSGVPS 80 Gaps ; 0 EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; COMPLEMENTARITY-DETERMINING 1. 78.1%; Score 710; DB 4; Length 108; 93.5%; Pred. No. 1.48e-140; COMPLEMENTARITY-DETERMINING COMPLEMENTARITY-DETERMINING 6; Mismatches 1; Indels SIEGELMAN M., CAPRA J.D.;
PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
-!- ANTI-ARSONATE HYBRIDOMA PROTEIN.
PIR; A01927; KVMAR. IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY. BY SIMILARITY

LT 2 KV5L MOUSE

21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
IG KAPPA CHAIN V. REGION (HP 123E6).
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; FRAMEWORK 1. COMPLEMENTARITY-DETERMINING 1. PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981). -!- ANTI-ARSONATE HYBRIDOMA PROTEIN. IMMUNOCLOBULIN V REGION; ANTIARSONATE ANTIBODY. 108 AA.

LT 3 KV5N_MOUSE

P01647;

RESULT ID KV AC P0 DT 21

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	άς 3.		108; 1s 0; Gans	terlbeame 60		0.7	27						AMMALIA;								NG 1.		NG 2.	NG 3.				.00	108;	ls 0; Gaps	ytsrlhsgvps 60		0.7	27	i
	complementarity-determining Framework 4. BY SIMILARITY.		DB 4; Length 108; .30e-138; ches 3; Indels	u i l [4st tobadat	utduckaessasasyu v. sec. aayusan yungyykkoy v.v.r.ryy ser. iisay ye 	rfsasasatdvsltisnleadiatvfcaavm]brtfaarkleik 107	RESGSGGTDYSLTINNLEOEDIATYFCOOGNTLPYFFGGGTKLEIN 127		108 AA.		ITE) DATE)		MOS MOSCULOS (MOUSE). EGNEANYOLOS, CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; FINITIONIA: COMMISSIONIA:				583 (1981).			TIBODY.	COMPLEMENTARITY-DETERMINING 1	2.	COMPLEMENTALIT-DETERMINING FRAMEWORK 3	COMPLEMENTARITY-DETERMINING		ITY.		7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	DB 4; Length 108; .24e-137;	ches 2; Indels	diqmtqtpsslsaslgdrvtiscrasqdinnylnwyrqkpdgtvklliyytsrlhsgvps		ort food blaik 1	RESOSSON SETTINAL EXPENSIVE CONTRACT FOR STATEMENT STATE	
FRAMEWORK 3	COMPLEMENTARI FRAMEWORK 4. BY SIMILARITY	MW; 64511 CN;	Score 701; Pred. No. 2 5: Mismat	al majoraca		diatvfcadavmlr	RFSGSGSGTDYSLTINNLEOEDIATYFCOOGNTLE	t t	PRT; 108	(TED)	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 01-0CT-1993 (REL. 27, LAST ANNOTATION UPDATE)	(HP 91A3).	TA; VERTEBRAT				SIEGELMAN M., CAFRA J.D.; PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981)	A PROTEIN.		IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY	COMPLEMENT	FRAMEWORK	COMP LEMENTY FRAMFWORK	COMPLEMENT	FRAMEWORK 4	BY SIMILARITY	MW; 62636 CN;	000	, 11		lscrasqdinnyln		odi et v foddana l	DIATYFCOGNTL	t t
88	97 108 88 108		77.1%; arity 92.5%; Conservative	i turbulaaa	848 1901 VC1	sltisnlede	SLT INNLEOE		STANDARD;	. 01, CREP	. 01, LAST	IG KAPPA CHAIN V-V REGION (HP 91A3)	(MOUSE). TAZOA; CHORDA	IA.			CAPRA J.D.; AD. SCI. U.S	E HYBRIDON	AI.	REGION; P	34	49	နို ಜိ	9.6	108	88 0			76.8%; tv 90.7%;	į,	lsaslgdrvt	SASLGDRVT	io]+ion]oc	SLTINNLEO	
57	D 23		SimiJ 99:	/	:	sasasatdv	SGSGSGTDY			1986 (REL	1986 (REL 1993 (REL	A CHAIN V	TA; METAZ	EUTHERIA; KODENTIA. [1]	E. A/J;	3	MAN M., CHI	II-ARSONAT	FIK; AU1927; KVMSAK HSSP; P01607; 1FAI.	SLOBULIN V	24	<u>ج</u> ج	2.5	68		100	Ε 1		Query Match Best Local Similarity	97; Cor	iqmtqtpss]	 OMTQTTSSI	Foggata	SGSGSGTD	
DOMAIN	DOMAIN DOMAIN DISULFID	SEQUENCE	Query Match Best Local					5	RESULT 5 ID KV50 MOUSE	21-JUL-	21-JUL- 01-0CT-	IG KAPP	EUKARYOTA; ME	(1)	SEQUENCE. STRAIN=A/J;	82150934	PROC. NATL. A	-!- ANT	HSSP; P	IMMUNOG	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DISULFID	SEQUENCE	1	Query Match Best Local	Matches	-	21 DJ	7	81	
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21-UUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
IG KAPPA CHAIN PRECURSOR V-V REGION (T1).
MUS MUSCULUS (MOUSE).
EUKRYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KV5E MOUSE
P01637;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30; Mismatches 18; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IG KAPPA CHAIN V-I REGION (DAUDI)
                                                                                                                                                                                                                                                                                                            EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 4.17e-115;
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KVII HUMAN STANDARD; PRT; 117 AA. P016Ū1;
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-MAY-1991 (REL. 18, LAST ANNOTATION UPDATE)
                                                                                                                                                                                    13-AUG-1987 (REL. 05, CREATED)
13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                       IG KAPPA CHAIN PRECURSOR V-I REGION (DAUDI).
                                                                                                                                          129 AA.
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85014148
KLOBECK H.G., COMBRIATO G., ZACHAU H.G.;
NUCLEIC ACIDS RES. 12:6995-7006(1984).
EMBL; X00966; HSVKQ2.
PIR; A01884; KIHUDI.
HSSP; P01607; IFGV.
IMMUNOGLOBULIN V REGION; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAMEWORK 3.
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Best Local Similarity 61.6%;
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                                                                                                                                            STANDARD;
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129 AA;
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123 gtkleik 129
                                            121 GTKLEIN 127
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121 GTKLE 125
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KV1X HUMAN
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128 AA.

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IG KAPPA CHAIN V-V REGION (T1). FRAMEWORK 1. COMPLEMENTARITY-DETERMINING 1. FRAMEWORK 2. COMPLEMENTARITY-DETERMINING 2.

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81052342 ALTENBURGER W., STEINMETZ M., ZACHAU H.G.; NATURE 287:603-607(1980).

SEQUENCE FROM N.A.

PIR; A01920; KVMST1. HSSP; P01607; 11IF. IMMUNOGLOBULIN V REGION; SIGNAL. SIGNAL 1 20

11) SEQUENCE FROM N.A. 81098966 BENTLEY D.L., RABBITTS T.H.; NATURE 288:730-733 (1980). [2] SEQUENCE FROM N.A.	D.L., RABBITTS T.H.; 181-189(1983). 0558; HSIGKZ. 881; KIHUII. 056; A21056. 1607; 1DFB. 0BULIN V REGION; SIGN 1 22 23 > 117 23 3 45 46 56	DOMAIN 51 11 FRAMEWORK 2. DOMAIN 72 78 COMPLEMENTARITY-DETERMINING 2. DOMAIN 79 101 FRAMEWORK 3. DOMAIN 111 >117 COMPLEMENTARITY-DETERMINING 3. DISULFID 45 110 BY SIMILARITY. NON TER 117 117 . SEQÜENCE 117 AA; 12799 MM; 78561 CN; QUERY MATCH 65.2%; Score 593; DB 4; Length 117; Best Local Similarity 72.1%; Pred. No. 3.24e-112; Matches 80; Conservative 17; Mismatches 14; Indels 0; Gaps	7 aqlıqıllıcfpgarcdiqmtqspsslsasvgdrvtitcrarqjisswlawyqqkpekap 66 :
[1] SEQUENC 8109896 BENTLEY NATURE [2] SEQUENC	BENTLEY CELL 32 EMBL; V PIR; A0 PIR; A2 PIR; A2 HSSP; P IMMUNOC SIGNAL CHAIN DOMAIN	DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DISULER NON TEE SEQUENC Query Matc Best Local	7 ac
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Gaps

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Indels

12; Mismatches 16;

79; Conservative

Matches

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61 rfsgsgsgtdftltidpmeeddtatyfcqqsrliprtfgggtkleik 107

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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE) IG KAPPA CHAIN V-I REGION (REI). 108 AA. PRT; 21-JUL-1986 (REL. 01, CREATED) STANDARD; HOMO SAPIENS (HUMAN). EUTHERIA; PRIMATES LT 14 KV10 HUMAN P01607;

HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 356:167-191(1975) X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) PALM W., HILSCHMANN N.; SEQUENCE. 16023758

EPP O., LATTMAN E.E., SCHIFFER M., HUBER R., PALM W.; BIOCHEMISTRY 14:4943-4952(1975). 76039968

PIR; A01873; KIHURE. PDB; IREI; 17-FEB-84. IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN; 3D-STRUCTURE. -!- THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER -!- THIS IS A BENCE-JONES PROTEIN.

COMPLEMENTARITY-DETERMINING 1. COMPLEMENTARITY-DETERMINING FRAMEWORK FRAMEWORK DOMAIN

FRAMEWORK 3. COMPLEMENTARITY-DETERMINING 3. FRAMEWORK 4 23 34 49 88 88 97 107 DISULFID NON TER STRAND DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN

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STRAND STRAND STRAND STRAND GRN

66412 CN; 11902 MW; 108 AA; SEQUENCE STRAND

62.0%; Score 564; DB 4; Length 108; Query Match

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                                         ö
                                                              1 digmtqspsslsasvgdrvtitcqasqdiikylnwyqqtpgkapklliyeasnlqagvps 60
                                                                            21 DIQMIQTISSLSASLGDRVTISCRASQDISSYLNWYQQRDGTIKLLIYYTSRLHSGVPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Mismatches 15; Indels 0; Gaps
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              IG KAPPA CHAIN V-I REGION (HK102). FRAMEWORK 1.
                                                                                                                                                                                                                  21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
IG KAPPA CHAIN PRECURSOR V-I REGION (HK102) (FRACMENT).
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAMEWORK 2. COMPLEMENTARITY~DETERMINING 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPLEMENTARITY-DETERMINING 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAMEWORK 3. COMPLEMENTARITY-DETERMINING 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 561; DB 4; Length 117;
Pred. No. 1.58e-104;
                            Pred. No. 3.01e-105;
16; Mismatches 13; Indels
                                                                                                            PRT; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12768 MW; 80156 CN;
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
81008966
81008966
BENTLEY D.L., RABBITTS T.H.;
NATURE 288:730-733(1980).
EMBL; Z00001, HSIGK3.
PIR; A01882; K.HU12.
HSSP; PO1607; JDFB.
IMMUNOGLOBULIN V REGION; SIGNAL.
SIGNAL.
                                                                                                                                                                      LT 15
KVIJ HUMAN STANDARD; 1
P01602;
21-JUL-1986 (REL. 01, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 61.7%;
Best Local Similarity 68.2%;
Matches 75; Conservative
                            Best Local Similarity 72.6%;
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    22

>117

45

56

71

78

110

>117
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117 1
117 AA;
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SEQUENCE
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Jul 8 08:21
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Search completed: Mon Jul 8 08:31:55 1996 Job time : 13 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Mon Jul 8 08:32:56 1996; MasPar time 4.21 Seconds 250.053 Million cell updates/sec Run on:

Tabular output not generated.

1 MVSSAQFLGLLLCFQGTRC..........CQQGNTLPYTFGGGTKLEIN 127 >US-08-137-117B-29 (1-127) from US08137117B.pep 909 Description: Perfect Score: Sequence: Title:

PAM 150 Gap 11 Scoring table:

70887 seqs, 8282111 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq22 i.part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14

Mean 30.127; Variance 164.919; scale 0.183 Statistics: Pred, No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.					2.20e-55			1.30e-52			3.16e-50	٠.,
Description	pPM-k3 protein produc	MAb SCH94.03 light ch	Anti-CD4 antibody MT	ME4 Light Chain V Reg	Mouse C4G1 Ig light-c	p146-k3 protein produ	Light (kappa) chain v	Mouse MAb 1C11 L chai	Human/murine IL-1 chi	Rat immunoglobulin L	KM641 H chain variabl	Murine anti-CD3 MAb U
ai	R28670	R84553	R32121	R09426	R39265	R29010	R12359	R12237	R47206	R33257	R53340	R30768
DB	9	14	9	S	œ	9	7	7	6	7	10	9
% luery Aatch Length DB								126				
% Query Match	100.0	96.7	96.4	94.6	93.8	90.9	90.0	89.9	89.5	88.2	86.5	77.9
Score	606	879	876	860	853	826	818	817	814	803	786	708
Result No.	1	7	3	4	5	9	7	œ	6	10	11	12

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3.61e-43	3.56e-42	6.04e-42	1.20e-40	5.86e-40	5.86e-40	2.01e-39	4.05e - 39	6.73e-38	1.36e - 37	1.93e - 37	2.74e - 37	2.74e-37	3.89e - 37	4.64e-37	6.59e-37	6.59e - 37	1.11e-36	1.58e - 36	3.80e - 36	7.67e-36	7.67e-36	9.14e - 36	1.09e - 35	2.19e - 35	6.27e-35	7.47e-35	7.47e-35	1.50e - 34	4.30e - 34		6.10e-34
Bispecific CD3-L6FvIg H5216-158 murine anti		Anti-influenza N10 sc	Feline immunoglobulin	puc-Rvh-PM1a.	pUC-RV1-PM1a.	Humanized 1308F VL.	CD4-specific CDR-graf	Completely humanised	pH52-9.0 humanised mu	Variable region of mu	pXOM2.	Anti-interleukin-1-al	Sequence of the leade	Sequence of the kappa	ME1-14 light chain va	Murine anti-human ath	KM-603 light chain.	Human anti-HBs light	Rat monoclonal antibo	Human V-kappa fragmen	Human V-kappa vk65.15	YFC51.1.1 light chain	huxCD3v9, humanised m	Light chain of 3D6 an	93KA9 anti-Varicella	Humanized antibody L2	CDR-grafted L243-gL2	Sequence of the VL re		Variable light chain	Humanized antibody L2
R60206 R30776	R47207	R52865	R11057	R29013	R29015	R57482	R13050	R43338	R30777	R06252	R30880	R75394	P30251	R38162	R60627	R62881	R53332	R42065	R81311	R38651	R62931	R30820	R30769	R20058	R65018	R64234	R64264	R54053	R47041	3	R64233
11	9	10	7	9	9	13	ო	_	9	-	9	13	4	7	12	12	2	œ	14	7	12	9	9	m	13	12	13	10	6	13	12
302	129	273	129	126	126	129	234	214	233	128	129	130	146	234	128	138	128	236	142	117	117	125	107	234	129	128	128	128	109	107	128
76.3	74.9	74.6	72.7	71.7	71.7	71.0	70.5	8.89	68.3	68.1	67.9	67.9	67.7	67.5	67.3			8.99	66.2	65.8	65.8	65.7	65.6	65.1	64.5	64.4	64.4	63.9	63.3	63.0	63.0
694	681	678	661	652	652	645	641	625	621	619	617	617	615	614	612	612	609	607	602	598	298	597	296	592	286	585	585	581	575	573	573
13	15	16	17	18	19	20	21	22	23	54	52	56	27	88	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALI GNMENTS

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used in example to illustrate the production of a human antibody which

The sequences given in R28670-71 were encoded by plasmids which were

recognises human interleukin-6 receptor (IL-6R). The antibody comprises light (L) chain and heavy (H) chain variable regions which were derived from a mouse monoclonal antibody produced from the hybridoma PMI which contained the plasmids pPM-k3 and pPM-h1. Sequence 127 AA;

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Gaps

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0; Indels

0; Mismatches

127; Conservative

Matches

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1 mvssaqflgllllcfqgtrcdiqmtqttsslsaslgdrvtiscrasqdissylnwyqqkp 60

Query Match 100.0%; Score 909; DB 6; Length 127; Best Local Similarity 100.0%; Pred. No. 1.06e-59;

Query Match

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	quence 131 AA;
Query Best Match	Query Match 96.7%; Score 879; DB 14; Length 131; Best Local Similarity 95.3%; Pred. No. 2.18e-57; Matches 121; Conservative 5; Mismatches 1; Indels 0; Gaps
	<pre>1 mmssaqflq1111cfqgtrcdiqmtqttsslsaslgdrvtiscrasqdisnylnwyqkp 60 : </pre>
	61 dgtvklliyytsrlhsgvpsrfsgsgtdysltisnlegediatyfcgggntlpwffgg 120
	121 gtkleik 127 21 GTKLEIN 127
SSULT R. R.	3 2121 standard; Protein; 127 AA. 2121; 2-JUN-1993 (first entry) rti-CD4 antibody MT 15.1 light chain variable r mmunosuppression; tissue transplantation; graff
	T-helper cell inhibition; transplant rejection; MAb; interleukin-2 receptor. Key Location/Qualifiers Peptide 120 /label= signal
ra na na na na	Region 21115 /label= Variable Region 116127 /label= J2
	28-JNN-1993. 30-DEC-1991; 143214. 25-JUL-1991; DE-124759. 30-DEC-1991; DE-143214. (BOEF) BOFRRINGER MANNHEIM GMBH. Kaluza B, Riethmueller G, Scheuer W, Weidle U; WPI; 93-037582/05.
~	N-PSDB; 036607. Synergistic antibody compsn. for use as immunosuppressant - comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R alpha- or anti-IL2R beta antibodies
m n n n n n n n n n n n n	Claim 5; Page 9; 18pp; German. This sequence is the light chain variable region of a preferred anti-CD4 monoclonal antibody for use in the claimed synergistic composition. MAD WT 15.1 is deposited as clone 15-1/P3/14 (ECACC 90090705). The anti-CD4 antibody is used with at least one anti-IL2R alpha or beta antibody. Individually the antibodies are strongly inhibiting and when used together their immunosuppressive properties are improved; they synergistically inhibit T-helper cell proliferation to effectively inhibit transplant rejection at low doses without significantly reducing the general immune response. See also Q36608-Q36616.
N Ber	Query Match 96.4%; Score 876; DB 6; Length 127; Best Local Similarity 92.9%; Pred. No. 3.72e-57; Matches 118; Conservative 7; Mismatches 2; Indels 0; Gaps h mmssaffalllefactradiamtatisslsssladavisarasadinnvlawadakn 60
2	^^ diff f: ^- f

Monoclonal antibody; MAb; SCH94.03; hybridoma; central nervous system;

.r 2 R84553 standard; Protein; 131 AA.

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02-FEB-1996 (first entry) MAb SCH94.03 light chain.

CNS; demyelination; multiple sclerosis; neural disease; therapeutic.

Location/Qualifiers

Region /label= Joining_region 129.131

Region 129..13 /label= C-kappa_region

W09530004-A1.

09-NOV-1995.

109..117

Region

70..76

/label= Leader_peptide Region 44..54

Peptide Mus sp.

/label= CDR1 'label= CDR2 /label= CDR3

Region

Region

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Hybridoma ATCC CR. 1167 was obtd. from a SJL/J mouse injected with spinal cord homogenate from a mammal uninfected with any demyelinating disease. The hybridoma produced a monoclonal antibody

Disclosure; Page 36-37; 63pp; English.

(SCH94.03) useful in promoting CNS remyelination. The SCH94.03 light chain amino acid sequence is given in R84553.

Monoclonal antibodies which stimulate central nervous system re-myelination - are produced by hybridoma ATCC CRL 11627, for treating multiple sclerosis, and viral or post-neural diseases of

Miller DJ, Rodriguez M; WPI; 95-393077/50. N-PSDB; T05311.

27-APR-1995; U05262. 29-APR-1994; US-236520. (MAYO-) MAYO FOUNDATION.

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Mus musculus WO9002569-A.

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WPI; 90-115825/15. N-PSDB; Q08608.

AC DDT AC

antigen

128 AA;

Sequence Query Match

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gtkleik 127

121 121

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p146-k3 protein product. Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H; heavy chain; variable region; mouse; monoclonal; hybridoma; AUK146-15; 9 9 Immunoglobulin; L-chain; platelet membrane glycoprotein; GPIIa/IIIb; monoclonal antibody; platelet agglutination; humanised antibody. Gaps įs protein - for treating disorders related to vascular thrombosis Compsn. contg. immunoglobulin specific for the GP-IIB and -IIIA ; 0 chain. See R39266 for the heavy chain sequence. The antibody specific for the CPIIa/IIIb protein and inhibits platelet agglutination. The Ig is thus useful in the treatment of This is the sequence of the mouse C4G1 immunoglobulin light Score 853; DB 8; Length 127; Pred. No. 2.20e-55; 7; Mismatches 3; Indels

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0; Gaps

N-PSDB; Q30759

Sequence

Matches

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W09219759-A. 12-NOV-1992

Protein

Synthetic.

Peptide

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1 mmssaqflgllllcfqgtrcdiqmtqttsslsaslgdrvtiscsasqgisnylnwyqqkp 60 New chimeric mouse human antibodies - used in treatment, diagnosis treatment, diagnosis and prophylaxis of HIV infections, and may be 1 mmssaqflgllllcfqgtrcdiqmtqttsslsaslgdrvtiscsasqgisnylnwyqqkp manipulating their respective joining (J) regions, to generate restriction enzyme recognition sites. The chimeric MAbs can be used as immunoconjugates, in association with e.g. toxins for HIV treatment. They can also be used in diagnosis of HIV. The mouse VL gene product may be used to produce chimeric mouse-human Abs against HIV-1 comprising human Ig constant regions and The chimeric MAbs are more effective than This is the light (kappa)- chain variable (V) region of a mouse monoclonal antibody (MAb), 1C11, and is specific for an HIV-1 viral antigen. It is used in the construction of a chimeric MAb comprising heavy and light chains having murine V regions and human C regions. The chimeric MAbs are more effective than murine MAb 1C11 since they have an increased compatibility in produced by a bacterial, yeast or mammalian expression system murine variable regions. These novel sequence are useful in humans. The heavy and light chain V-regions are joined by Length 126; Score 818; DB 2; Length 127; Pred. No. 1.09e-52; 7; Mismatches 7; Indels Score 817; DB 2; Length 126 Pred. No. 1.30e-52; 6; Mismatches 7; Indels Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR; Disclosure; Fig 13; 108pp; English. and prophylaxis of HIV infections. JT 8 R12237 standard; Protein; 126 AA. 19-AUG-1991 (first entry) Mouse MAb 1C11 L chain V region. Match 89.9%; Local Similarity 89.7%; Nes 113; Conservative Query Match 90.0%; Best Local Similarity 89.0%; Matches 113; Conservative 13-NOV-1989; US-433703. 13-NOV-1990; U06627. WPI; 91-178106/24. (XOMA-) Xoma Corp. ||||||: 121 GTKLEIN 127 121 gtkleik 127 N-PSDB; Q12017. HIV-1; chimera. WO9107494-A. 30-MAY-1991. Sequence Query Match Sequence Best Loca Matches g ð g 염 888888888888888 요 ð ð δ ö used in example to illustrate the production of a human antibody which recognises human interleukin-6 receptor (IL-6R). The antibody comprises light (1) chain and heavy (H) chain variable regions which were derived from a mouse monoclonal antibody produced from the hybridoma AUKI46-15 which contained the plasmids p146-K3 and p146-h1. 61 dgtvklliydtsrlhsgvpsrísgagsgtdysltisnlegediaayfcgggytpwtfgg 120 61 DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120 1 mvstpqflgllvicfqgtrcdiqmtqttsslsaslgdrvtiscrasqdisnylnwyqqkp 60 1 MYSSAQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP 60 0; Gaps 15-AUG-1991 (first entry) Light (kappa) chain variable region of murine 1C11 immunoglobulin. Chimeric antibodies; immunoconjugates; HIV; AIDS. has low antiqenicity and contains mouse V-region complementarity The sequences given in R29010-11 were encoded by plasmids which New chimeric mouse-human antibodies - used to detect, kill and Reconstituted human antibody to human interleukin-6 receptor Score 826; DB 6; Length 127; Pred. No. 2.65e-53; 4; Indels Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR; WPI; 91-178044/24. Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M; WPI; 92-398882/48. Mismatches Disclosure; Page 127-128; 207pp; Japanese. Location/Qualifiers Disclosure; fig 13; 107pp; English R12359 standard; Protein; 127 AA. remove HIV-1 antigen from sample Query Match

Best Local Similarity 89.8%; 114; Conservative plasmid; p146-k3; p146-h1 (CHUS) CHUGAI SEIYAKU KK GREEN CROSS CORP US-433730. 24-APR-1992; J00544. 25-APR-1991; JP-095476. 19-FEB-1992; JP-032084. /note= "Signal peptide" 21..127/note= "Mature peptide" 13-NOV-1990; U06615. determining regions

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Gaps

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(XOMA-) XOMA CORP.

(GREC)

13-NOV-1989;

Mus musculus.

R12359;

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WO9107493-A. 30-MAY-1991. N-PSDB; Q12061.

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N-PSDB; Q5606

03-FEB-1994

Protein Peptide

Synthetic.

sites in vivo

Sequence Query Match

Matches

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ö variable regions respectively. The DNA sequences encoding these proteins were used in the construction of humanised chimeric antibody DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120 dgtvkllifyssnlhsgvpsrfsgggsgtdysltisnlepediatyfchgysklpwtfgg 120 9 IKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGGGTK 123 The sequences given in R33256-57 represent rat heavy and light chain have been changed. 0; Gaps expression vectors. In these humanised antibodies none of the amino 1 mmssaqflgllllcfqgtrcdiqmtqtassllaslgdrvtiscsasqdisnylnwyqqkp 12-JUL-1993 (first entry)
Rat immunoglobulin L chain varible region of pKM641LA2.
Promoter; variable; region; rat; immunoglobulin; heavy; H; chain; humanised; chimeric; antibody; expression vector. Humanised chimeric antibody prodn. against ganglioside GD3 - for Monoclonal antibody; Ab; ganglioside GM2; chimera; chimeric antibody; expression vector; heavy; light; chain; hypervariable region; CDR; constant region; hybridoma; 88.2%; Score 802; DB 7; Length 128; 85.8%; Pred. No. 1.86e-51; Atlive 11; Mismatches 7; Indels (KYOW) KYOWA HAKKO KOGYO CO LTD. Hanai N, Hasegawa M, Kuwana Y, Miyaji H, Shitara K, treating cancers, such as melanoma, neuroblastoma, etc. Claim 6; Page 30-31; 63pp; English. acids of the non-human animal Ab variable region Sequence 128 AA; Location/Qualifiers .T 10 R33257 standard; Protein; 128 AA. Ä.

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terminus of the VL-VH fusion cassette was fused at the Sall site to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domain at the BclI site and/or to a short "helical" peptide linker to construct the bispecific CD3-L6FvIg antibody derivative. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    variable regions for L6 were fused in frame to the opposite end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       carboxy-terminus was fused directly to the hinge region of the Fc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amplified by PCR methods. A gene fusion was constructed from the two amplified domains and a (Gly4Ser)3 linker. The amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expression vector encoding bispecific fusion protein - having binding domains for separate targets joined by helical peptide, useful e.g. for diagnosis and treatment Example 1; Fig 11 and Page 29-31; 50pp; English.

The VL and VH sequences of the anti-CD3 hybridoma G19-4 were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the 16 light chain variable region leader peptide and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the helical linker (not included in R60206).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 94-250885/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              302 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; Q81076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= hinge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-AUG-1994.
                                                                                                                                                                                                                                                                                                                                                                                                           14-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP-610046-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Linsley PS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGATLPYTFGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 dgtvkllifyssnlhsgvpsrfsgggsgtdysltisnlepgdiatyfchqysklpwtsgg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 mmssaqflg11111cfqgtrcdiqmtqtasslpaslgdrvtiscsasqdisnylnwyqqkp 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Numanisation of antibodies - by molecular modelling of the variable
                                                                                                                                                                                                                                                                                                                          Reference example 2; Page 115-116; 191pp; English.
Example 2 describes the construction of the vector pChi641HA1
                                                                                                                                                                                                                                                                                                                                                                   for chimeric human antibody H chain expression. mRNA from mouse anti-GD3 monoclonal Ab KM641-producing cells
                                                                                                                                                                                                                                                                                                                                                                                                                              The base sequences of the Ig variable regions in KM641
H chain cDNA (pKM641HA3) and KM641 L chain cDNA (pKM641LA2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 786; DB 10; Length 128;
Pred. No. 3.16e-50;
                                                                                                                                                                                                                                                           Humanised antibody specific for ganglioside GM2 - used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Indels
                                                                                                                                                                                                                                                                               producing a cytocidal effect on cancers such as melanoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    are given in Q45438-39. A KM641-derived chimeric human Ab H chain expression vector was constructed by joining the H chain variable region gene from pKM641HA3 to a vector for chimeric human Ab H chain expression using
                                                                                                                                                                               Hasegawa M, Koike M, Kuwana Y, Nakamura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAY-1993 (first entry)
Murine anti-CD3 MAb UCHT1 light chain variable domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domains and alteration by gene conversion mutagenesis
                                                                                                                                                                                                                                                                                                                                                                                                             was isolated and KM641 H and L chain cDNAs isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Humanisation; rapid; monoclonal antibody; muxCD3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the synthetic DNAs given in Q63439 and Q63440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Mismatches
                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 5; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LT 12
R30768 standard; protein; 107 AA.
                                                                                                                                                          (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 86.5%;
Best Local Similarity 84.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107; Conservative
                                                                                                                                                                                                                                                                                                         neuroblastoma and glioma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-JUN-1991; US-715272.
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                                                                                                                                     07-SEP-1992; JP-238452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carter PJ, Presta LG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-1992; U05126.
                                                                                                                    07-SEP-1993; 046181.
                                                         /label= sig peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 93-018139/02.
                                                                                                                                                                                                                     WPI; 94-126857/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTKLEIN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 gtkleik 127
                                                                                                                                                                                                                                              N-PSDB; 045438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09222653-A.
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-DEC-1992
                                                                            AU9346181-A
                                                                                                 17-MAR-1994
                                                                                                                                                                                                    Shitara K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                               Hanai N,
                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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1 digmtgttsslsaslgdrvtiscrasgdirnylnwyggkpdgtvklliyytsrlhsgvps 60 21 DIQMIQTISSLSASLGDRVIISCRASQDISSYLMWYQQKPOGTIKLLIYYTSRLHSGVPS 80 Gaps The sequence is that of the light chain variable domain of murine anti-CD3 monoclonal antibody UCHTI (muxCD3, Shalaby 1992). Ledbetter JA; fusion protein; recombinant bispecific single chain antibody; helical peptide linker; anti-16 antibody; tumour cell antigen; anti-CD3 antibody; variable region. ; 0 Length 107, 2; Indels Bajorath J, Fell PH, Gilliland LK, Hayden MS, Score 708; DB 6; 1 Pred. No. 3.06e-44; 6; Mismatches Bispecific CD3-L6FvIg antibody derivative. Location/Qualifiers R60206 standard; Protein; 302 AA. (BRIM) BRISTOL-MYERS SQUIBB CO. Query Match 77.9%; Best Local Similarity 92.5%; Matches 99; Conservative (first entry) 'label= (Gly4Ser)3_linker /label= Fv_helical_linker 275..302 134..148 /label= CD3_VL-VH_fusion 24..271 31-JAN-1994; 300692. 01-FEB-1993; US-013420. 13-SEP-1993; US-121054. /label= L6_VL_leader

76.3%; Score 694; DB 11; Length 302;

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2

US-08-137-117B-29.rag

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Best Local Similarity 93.3%; Pred. No. 3.61e-43; Matches 97; Conservative 3; Mismatches 4; Indels 0; Gaps	24 diqmtqttsslaaslgdrvtiscrasqdirnylnwyqqkpdqtvklliyytsrlhsgvps 83 	84 rfsgsgsgtdysltianlgpediatyfcgggntlpwtfgggtkl 127 	RESULT 14 ID R30776 standard; protein; 214 AA.			~	domains and alteration by gene conversion mutagenesis Disclosure; Fig 6B; 126pp; English. The sequence is that of the light chain of murine antibody H52L6-158. Sequence 214 AA;	Query Match 75.5%; Score 686; DB 6; Length 214; Best Local Similarity 88.8%; Pred. No. 1.48e-42; Matches 95; Conservative 10; Mismatches 2; Indels 0; Gaps	<pre>1 dvqmtqttsslsaslgdrvtincrasqdinnylnwyqqkpngtvklliyytstlhsgvps 60 </pre>	61 rfsgsgsgtdysltisnldgediatyfcgggntlpptfgggtkveik 107 	Ing					/note= "Signal		WO9402627-A. 03-FEB-1994.
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Search completed: Mon Jul 8 08:33:13 1996

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121

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g δ

1 msvptqvlgllllwltdarcdiqmtqspsslsasvgdrvtitcrtsqdinnnlnwyqqtp 60

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of a human antibody and the variable region is from a mouse anti-human IL-1 antibody or is a mouse-human graft containing the CDR regions of
                                                                                                                                                                                                                                              Claim 2; Fig 10; 58pp; Japanese. The sequences given in R47205-08 represent the light and heavy chain, variable and constant regions of a chimeric recombinant antibody against human interleukin-1 (IL-1). The antibody has a light (L) chain in which the constant region is that of a human antibody and the variable region is from a mouse anti-human IL-1 antibody or is a
                                                                                                                                                                                                                                                                                                                                                                                                      mouse-human graft containing the CDR regions of mouse anti-human IL-1 antibody, and a heavy (H) chain in which the constant region is that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mouse anti-human IL-1 antibody,. The chimeric antibody is used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treat diseases in which abnormal amounts of IL-1 are produced, eg.
                                                                                                                                                                                                    abnormal, and for diagnostic imaging of interleukin-1 production
                                                                                                                                                   Mouse/human chimeric antibody against human interleukin-1 - for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inflammatory disease, arteriosclerosis, diffused intravascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coagulation or leukemia. It can also be labelled and used for diagnostic imaging of IL-1 producing sites in vivo. Sequence 129 AA;
                                                                                                                                                                               treatment of diseases in which production of interleukin-1 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 681; DB 9; Length 129;
Pred. No. 3.56e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19; Mismatches 15; Indels
                                              (SAKA ) OTSUKA PHARM CO LTD.
Hirai Y, Nishida T, Omoto Y, Owens RJ;
WPI; 94-048885/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 74.9%;
Best Local Similarity 73.0%;
Matches 92; Conservative
08-JUL-1993; J00941.
16-JUL-1992; JP-189248.
                                                                                                                           N-PSDB; Q56068
                                                                                                                                                                                                                              sites in vivo
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

Mon Jul 8 08:34:20 1996; MasPar time 8.84 Seconds 391.433 Million cell updates/sec Run on:

protein - protein database search, using Smith-Waterman algorithm

MPsrch_pp

Tabular output not generated.

>US-08-137-117B-31 (1-137) from USO8137117B.pep 1002 1 MRVLILIMLFTAFPGILSDV......LARTTAMDYWGQGTSVTVSS 137

Description: Perfect Score:

Sequence:

PAM 150 Gap 11 Scoring table:

82306 seqs, 25270970 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4 8:unann5 9:unann6 10:unann7 11:unann8 12:unrev1 13:unrev2

Mean 42.150; Variance 133.880; scale 0.315 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	3.01e-89	2.46e-88	2.61e-81	1.57e-80	1.51e-77	2.04e-77	2.22e-76	1.79e-75	1.44e-74	1.25e-72	3.06e-68	1.11e-68
Description	Ig heavy chain precu 3	Ig heavy chain precu 2	Iq heavy chain precu 2	Ig heavy chain precu 1	Ig heavy chain precu 1	Iq heavy chain V req 2	monoclonal antibody 2	Ig heavy chain V reg 1	Iq heavy chain precu 1	Iq heavy chain V req 1	Ig mu chain precurso 3	Ig heavy chain V reg 4
ID	s30752	PL0100	B24672	HVMS1B	AVMS35	507637	c53285	128195	HVMS31	S38718	D33932	S26464
* Query Match Length DB	149 5	135 5	134 5	116 2	137 2	136 5	119 11	117 11	116 2	116 5	115 11	106 5
% Query Match	83.3	85.6	77.2	9.9/	74.4	74.3	73.5	72.8	72.1	70.6	67.2	67.1
Score	835	828	774	168	745	744	736	729	722	707	673	672
Result No.	1	2	e	4	5	9	7	80	6	10	11	12

1 070-66	1 150 65	2.79e-65	. 23e-	7.23e-64	1.03e-62	8.17e-62	1.56e-60	5.08e-60	5.08e-60	6.83e-60	1.44e - 56	1.12e-55	1.51e-55	2.71e-55	4.88e-55	2.11e-54	7.11e-53	7.11e-53	9.53e-53	2.29e-52	5.52e-52	5.52e-52	9.90e-52	7.66e-51	2.46e-50	7.92e-50	1.06e-49	1.06e-49	1.90e-49	1.90e-49	2.54e-49	3.40e-49
hount chain W	J. Laha	chain	heavy chain	heavy chain V	heavy chain V re	heavy chain -	Ig heavy chain V reg	Ig heavy chain V reg	heavy chain V	Ig heavy chain V reg	heavy chain V	heavy chain V	Ig heavy chain V reg	heavy chain V	Iq heavy chain V req	Ig heavy chain V reg	heavy chain V	Ig heavy chain precu	Ig heavy chain V reg	heavy chain -		Ig heavy chain V reg	heavy chain -	Ig heavy chain V reg	Ig heavy chain V reg	Ig mu heavy chain V	þe	Iq mu heavy chain V	Iq heavy chain precu	mu heavy cha	þea	pothetical hybr
121 13 637200	177	117 2 HVMS73	115 11 F25114	2	Ξ	123 11 S42771	104 5 S26467	7	11	120 11 A25114	ഹ	147 13 S13519		2	13	102 11 514486	13 5316		Ξ	2	Ξ	139 13 \$31586	ß	5 524	2	11 S	13 5		ııı		13 513	
661 66 0		64.	64.		630 62.9				_		582 58.1			-,	570 56.9	ß	553 55.2	S	55.	54.	546 54.5	54.	54.	53.	53.	52.	2	52.	52.	52.	52.	52.
13	2 -	15	16	11	18	19	20	21	22	23	24	25	56	27	. 58	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT

ENTRY	S30752 #type complete
TITLE	Ig heavy chain precursor V region - mouse
ORGANISM	#formal name Mus musculus #common name house mouse
DATE	31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Sep-1995
ACCESSIONS	530752
REFERENCE	530751
#authors	Grant, F.J.; Levin, S.D.; Gilbert, T.; Kindsvogel, W.
# journal	Nucleic Acids Res. (1987) 15:5496
#title	Improved RNA sequencing method to determine immunoglobulin
	mRNA sequence.
#accession	S30752
##molecule type mRNA	type mRNA
##residues	1-149 ##label GRA
##cross-re	#‡cross-references EMBL:X05878
CLASSIFICATION	#superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS	immunoglobulin
FEATURE	
138-149	#domain C region (C-gamma 2b) (fragment) #status
	predicted #label CRE
SUMMARY	#length 149 #molecular-weight 16635 #checksum 9814
Query Match	83.3%; Score 835; DB 5; Length 149;
Best Local Sim	; Pred. No. 3.01e-89;
Matches 116; Conservative	Conservative 7; Mismatches 14; Indels 0; Gaps 0;

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ORGANISM

this sequence belongs to the VH3660 subfamily fsuperfamily immunoglobulin V region; immunoglobulin homology

immunoglobulin

amino acid sequence is not given

1-116 ##label LEV

#domain signal sequence #status predicted #label SIG\

Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J. J. Exp. Med. (1989) 169:2007-2019

JT0501

 J_{10508}

Early onset of somatic mutation in immunoglobulin VH

during the primary immune response.

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Ig heavy chain precursor V region (1843) - mouse #formal name Mus musculus #common name house mouse 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 18-Feb-1995

#type complete

HVMS1B

##experimental_source strain BALB/cJ cross-references MUID:89279149 ##molecule type mRNA ##residues CLASSIFICATION #accession ##note finote *authors journal ACCESSIONS title REFERENCE ORGANISM KEYWORDS SUMMARY FEATURE RESULT TITLE ENTRY DATE 셤 g 셤 õ ð ð #superfamily immunoglobulin V region; immunoglobulin homology Near, R.I.; Haber, E. Mol. Immunol. (1989) 26:371-382 Characterization of the heavy and light chain immunoglobulin variable region genes used in a set of anti-digoxin ;; the VH40-140 gene segment is classified as a member of SIG 61 gnklewmayihysgntdfnpslksrisitrdtsknqfflqlnsvtaedtatyycargygn 120 61 GNKLEMMCYISYSGITTYNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLAR 120 61 gnrlewmgyityngyttynpslksrfsitrdtsknqlflqlssvttedtatyycarsyd- 119 9 1 MRVLILAMIFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSTSTTSDHAMSMIRQFP 60 Ig heavy chain precursor V region (40-140) - mouse #formal name Mus musculus #common name house mouse 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 3; Gaps 1 mrvlillwlftafpgglsdvqlqesgpglvkpsqslsltctvtgysitsdyawswirqfp #domain signal sequence #status predicted #label #domain V segment #status predicted #label VRE\
#domain D segment #status predicted #label DRE\
#domain J segment #status predicted #label JRE #molecular-weight 15303 #checksum 9859 Ig heavy chain precursor V region (VGAM3-2) - mouse #formal_name Mus musculus #common_name house mouse Length 135; Indels .**,** Score 828; DB 5; 1 Pred. No. 2.46e-88; 9; Mismatches the 36-60 VH gene family #type complete #type complete 1-135 ##label NEA ##experimental_source strain A/J #cross-references MUID:89238344 Query Match 82.6%; Best Local Similarity 84.7%; 120 -y-fdywgggttltvss 134 121 TTAMDYWGQGTSVTVSS 137 121 yyamdywgqgtsvtvss 137 121 TTAMDYWGQGTSVTVSS 137 116; Conservative 12-Apr-1995 antibodies #length 135 #molecule type DNA B24672 PL0100 PL0100 PL0100 PL0100 ##residues #introns CLASSIFICATION #accession ##note *authors | journal 119-135 117-118 **ACCESSIONS** Matches #title 19-115 REFERENCE ORGANISM GENETICS FEATURE RESULT ENTRY RESULT ENTRY DATE

#superfamily immunoglobulin V region; immunoglobulin homology 5; 61 GNKLEMMGYISYSGITTYNPSIKSRISITRDTSKNQFFLQINSVTTGDTSTYYCARSLAR 120 this sequence was determined from the differentiated 61 gnklewmgyihysgstnynpslksrisitrdtsknqfflqlnsvttedtatyycaryyd- 119 Gaps 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change #product Ig heavy chain V region VGAM3-2 #label
#length 134 #molecular-weight 15254 #checksum 6268 3; Length 134; 3; Mismatches 18; Indels ö #authors Winter, E.; Radbruch, A.; Krawinkel,
#journal EMBO J. (1985) 4:2861-2867
#cross-references MUID:86055722 Score 774; DB 5; 1 Pred. No. 2.61e-81; 1-134 ##label WIN Best Local Similarity 82.5%; 77.28; 120 -y-faywgqgtlvtvsa 134 121 TTAMDYWGQGTSVTVSS 137 113; Conservative 31-Dec-1993 ##molecule_type DNA A91022 B24672 ##residues #introns CLASSIFICATION accession Query Match ##note Matches ACCESSIONS 9-134 REFERENCE

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activity.

#superfamily immunoglobulin V region; immunoglobulin homology
#length 136 #molecular-weight 15307 #checksum 182 #superfamily immunoglobulin V region; immunoglobulin homology #domain signal sequence #status experimental #label SIG\ ö #product Ig heavy chain V region (MOPC 315) #label MAT\ 19-52, 'K', 53-75, 'BYGB', 80-101, 'D', 103-106, 'ZB', 109-122, the authors translated the codon TAT for residue 112 a Ile, TAC for residue 113 as Ile, and TAC for residue 61 GNKLEMMGYISYSGITTYNPSIKSRISITRDTSKNQFFLQINSVTTGDTSTYYCARSLAR 120 61 gnklewlgfikydgsngynpslknrvsitrdtsenqfflklnsvttedtatyycagdndh 120 the expressible VH gene from a hybridoma 1 mkvlsllylltaipgimsdvqlqesgpglvkpsqslsltcsvtgysitsgyfwnwirqfp 60 1 MRVLILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFP 60 Gaps #formal_name Mus musculus #common name house mouse 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Oct-1994 #length 137 #molecular-weight 15399 #checksum 2186 = = = ô producing monoclonal antibodies against porcine fdomain immunoglobulin homology flabel IMM Score 745; DB 2; Length 137; Pred. No. 1.51e-77; 14; Mismatches 22; Indels Urakov, D.N.; Deev, S.M.; Polyanovsky, O.L. Nucleic Acids Res. (1989) 17:9481 The structure of the expressible VH gene fr Ig heavy chain V region (PTF.02) - mouse 124-137 ##label FRA #type complete anti-dinitrophenyl activity. 1-136 ##label URA ##cross-references EMBL:X16740 cross-references MUID:90067954 Query Match 74.4%; Best Local Similarity 73.7%; 121 lyyfdywgggttltvss 137 121 TTAMDYWGQGTSVTVSS 137 transferrin. 101; Conservative ##molecule_type protein ##molecule_type DNA 507637 507637 507637 507637 15/1 #introns CLASSIFICATION SUMMARY

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US-08-137-117B-31.pgr

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*accession Query Match #note authors journal journal Matches ACCESSIONS title title 19-116 33-116 REFERENCE ORGANISM KEYWORDS FEATURE SUMMARY SUMMARY RESULT ENTRY DATE 임 3 쇰 셤 ð g à ð 128195 #type complete
Ig heavy chain V region (anti-haloperidol antibody D) - mouse
#formal name Mus musculus #common name house mouse
01-Dec-1989 #sequence_revision 30-Sep-1991 #text_change : antibodies: primary structures of the variable regions of seven antibodies specific for 17 alpha-hydroxyprogesterone 5; Sawada, J.; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Mol. Immunol. (1991) 28:1063-1072 61 npslksrisltrdtsknqfflqlnsvttedtatyycsrg-nryyyamdywgqgtsvtvss 119 61 gnklewmgyisydgsngynpslknrisitrdtsknqfflklnsvttedtatyyctrg-dg 119 61 GNKLEWMGYISYSGITTYNPSIKSRISITRDTSKNQFFIQIMSVTTGDTSTYYCARSLAR 120 19 NPSIKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLARIT-AMDYWGQCTSVTVSS 137 1 mkvlsilylltaipgilstvqlqesgpglvkpsqslsltcsvtdfsitsgyywhwirqfp 60 Gaps Gaps monoclonal antibody OHP7D7.2.3=heavy chain variable and joining region - mouse (fragment) #formal name Mus musculus #common name house mouse 02-May-1994 #sequence_revision 18-Nov-1994 #text_change or 11-deoxycortisol and their pH-reactivity profiles. $\mbox{\it fcross-references}$ MUID:92017897 Molecular characterization of monoclonal anti-steroid 10; Mismatches 23; Indels 1; 5; Score 736; DB 11; Length 119; Pred. No. 2.22e-76; Score 744; DB 5; Length 136; Pred. No. 2.04e-77; Indels sequence extracted from NCBI backbone Sherman, M.A.; Deans, R.J.; Bolger, M.B. 6 7; Mismatches ##cross-references NCBIN:63297; NCBIP:63302 #length 119 #checksum 2281 #type fragment 74.3%; Query Match 73.5%; Best Local Similarity 85.0%; 120 yhfftywgqgtlvtvsa 136 121 TTAMDYWGQGTSVTVSS 137 102; Conservative 103; Conservative 23-Mar-1993 18-Nov-1994 Best Local Similarity 128195 C53285 A28195 #accession Query Match finote **f**authors **fauthors** #journal ACCESSIONS Matches ACCESSIONS Matches TITLE ORGANISM #title REFERENCE REFERENCE ORGANISM SUMMARY RESULT ENTRY ENTRY TITLE DATE 셤 염 g ð 염 ð g ð ð 8

#superfamily immunoglobulin V region; immunoglobulin homology ö ; the authors translated the codon AAC for residue 61 as Thr, and did not translate the codon ACT for residue Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J. J. Exp. Med. (1989) 169;2007-2019

Early onset of somatic mutation in immunoglobulin VH genes Haloperidol binding to monoclonal antibodies. Hypervariable 8 19 DVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAMSMIRQFPGNKLEMMGYISYSGITTY 78 1 mkvlsllylltaipgilsdvqlqesgpglvkpsgslsltcsvtgysitsgyywnwirgfp 60 Gaps Gaps Ig heavy chain precursor V region (M315) - mouse #formal name Mus musculus #common name house mouse 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 1 dvqlqesgpglvkpsqslsltctvtgysitseyawnwirqfpgnklewmgyisysgttsy #domain signal sequence #status predicted #label #product Ig heavy chain V region (M315) #status predicted #label MAT\ 66 as Thr #length 117 #molecular-weight 13023 #checksum 9723 ; 0 5; #length 116 #molecular-weight 13095 #checksum #domain immunoglobulin homology #label IMM Length 117; 72.1%; Score 722; DB 2; Length 116; 83.6%; Pred. No. 1.44e-74; 7; Mismatches 12; Indels 8; Indels region amino acid sequence determination. amino acid sequence is not given during the primary immune response cross-references MUID:89279149 (1988) 263:4059-4063 Score 729; DB 11; Pred. No. 1.79e-75; 7; Mismatches #type complete ##experimental_source strain BALB/cJ 1-117 ##label SHE 1-116 ##label LEV ##cross-references GB:M19775 ##note the authors t Query Match 72.8%; Best Local Similarity 85.7%; Best Local Similarity 83.6%; Matches 97; Conservative immunoglobulin 102; Conservative 18-Feb-1995 ##molecule_type mRNA ##molecule_type mRNA JT0509 JT0501 HVMS31 128195 JT0509 ##residues #fresidues CLASSIFICATION accession

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Avrameas, S.
Proc. Natl. Acad. Sci. U.S.A. (1989) 86:4624-4628
Two murine natural polyreactive autoantibodies are encoded by
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61 GNKLEWMGYISYSGITTYNPSLKSRISITRDTSKNQFFLQLMSVTTGDTSTYYCAR 116 US-08-137-117B-31.pg Jul 8 08:24

#superfamily immunoglobulin V region; immunoglobulin homology
#length 106 #molecular-weight 11960 #checksum 8356 1; 5; 61 npslknrisitrdtsknqfflklnsvttedtatyycarggiygyddyfdswgggttltvs 120 79 NPSIKSRISITRDISKNØFFLQINSVTTGDISTYCARS-L-ARTTAMDYWGQGISVTVS 136 9 19 DVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAMSWIRQEPGNKLEMMGYISYSGITTY 78 Gaps Gaps 337200 #type complete
Ig heavy chain V region - mouse
#formal name Mus musculus #common_name house mouse
10-Dec-I993 #sequence_revision 10-Dec-1993 #text_change 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 1 dvqlqesgpglvkpsqslsltcsvtgysitssyywnwirqfpgnklewmgyisydgrndy Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Ig heavy chain V region - mouse fformal name Mus musculus fcommon name house mouse 2; ; ##etatus preliminary #fresidues 1-121 ##label FIS ##cross-references EMBL:X74587 :Y #length 121 #molecular-weight 13739 #checksum Ouery Match 66.0%; Score 661; DB 13; Length 121; Best Local Similarity 77.7%; Pred. No. 1.07e-66; Matches 94; Conservative 9; Mismatches 16: Tandla submitted to the EMBL Data Library, August 1993 Score 672; DB 5; Length 106; Pred. No. 4.11e-68; ravaler, J. submitted to the EMBL Data Library, April 1991 5; Indels 61 dtsknqfflqlnsvttedtatyycarg-gwlppleywgqgttltvss 106 91 DISKNOFFLOLMSVITGDISTYYCARSLARTTAMDYWGGGISVIVSS 137 11; Mismatches #type complete 1-106 ##label KAV ##cross-references EMBL:X59114 preliminary Query Match 67.1%; Best Local Similarity 84.1%; 90; Conservative Kreuzaler, F. 12-Apr-1995 Kavaler, J. ##molecule_type mRNA S26464 \$26464 526464 526459 537200 S37200 **S37200** ##residues ##residues CLASSIFICATION 121 s 121 submission ##status #submission *accession accession 12 13 **f**authors #authors **ACCESSIONS** Matches ACCESSIONS REFERENCE REFERENCE ORGANISM ORGANISM SUMMARY RESULT RESULT TITLE ENTRY DATE DATE g 쇰 셤 염 g δ ð à δ ð

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Mon Jul 8 08:33:31 1996; MasPar time 4.97 Seconds 422.613 Million cell updates/sec Run on:

Tabular output not generated.

Description: Perfect Score:

>US-08-137-117B-31 (1-137) from US08137117B.pep 1002 1 MRVLILIMLFTAFPGILSDV......LARTTAMDYWGQCTSVTVSS 137 Sequence:

PAM 150 Gap 11 Scoring table:

43470 seqs, 15335248 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot31
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8

Database:

Mean 42.978; Variance 84.975; scale 0.506 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

PRT; 116 AA.	TED)	LAST SEQUENCE UPDATE)	JI-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)	region (1943):	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;						LEVY N.S., MALIPIERO U.V., LEBECQUE S.G., GEARHART P.J.;	(1989).	-!- THIS SEQUENCE BELONGS TO THE VH3660 SUBFAMILY.			SIGNAL.		IG HEAVY CHAIN V REGION (1843).	FRAMEWORK 1.	COMPLEMENTARITY-DETERMINING 1.	FRAMEWORK 2.	COMPLEMENTARITY-DETERMINING 2.	FRAMEWORK 3.	BY SIMILARITY.
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FRANCIS S.H., LESLIE R.G.O., HOOD L., EISEN H.N.; FRANCIS S.H., LESLIE R.G.O., HOOD L., EISEN H.N.; PROC. NATL. ACAD. SCI. U.S.A. 71:1123-1127(1974). DR FINAL SCI. U.S.A. 71:1123-1127(1974). DR FINAL SCI. U.S.A. 71:1123-1127(1974). DR FINAL F.D.		.6.	S & S	STRAIN=BAI 89279149	B/CJ;	i
53 RW HSS RW RW RW RW RW RW RW		LIE R.G.Q., HOOD L., EISEN H.N.; SCI. U.S.A. 71:1123-1127(1974).	R. R. P.	J. EXP. ME PIR; JT050	MALIPI D. 169: 9; HVMS	200 31.
MARCOLIES M.N., GIVOL D., ZAKUT R.;			E E	HSSP; P018 IMMUNOGLOB	25; 1BA ULIN V	F. 88
PADIAN E.A., DAVIES D.R., PECHT I., GIVOL D., WRIGHT C.; PADIAN E.A., DAVIES D.R., PECHT I., GIVOL D., WRIGHT C.; PADIAN E.A., DAVIES D.R., PECHT I., GIVOL D., WRIGHT C.; PADIAN E.A., DAVIES D.R., PECHT I., GIVOL D. 41:627-637(1977). PATIAN MAS ISOLATED FROM A MYELOMA PROTEIN THAT HAS PATIAN MAS ISOLATED FROM A MYELOMA PROTEIN THAT HAS PATIAN PROTEIN PROTEIN THAT HAS PATIAN PROTEIN PROTEIN THAT HAS PATIAN PROTEIN PRO		S. M.N., GIVOL D., ZAKUT R.;	1 1 1 1	CHAIN	19	116
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CHARACTERISTIC OF THE ANTIARSONATE RESPONSE OF STRAIN A/J MICE HSSP, P01825; 1HFM. IMMUNOGLOBULIN V RECION; ANTIARSONATE ANTIBODY. 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE) 117 AA. 144 AA. IG HEAVY CHAIN PRECURSOR V REGION (MOPC 141) SEQÜENCE 144 AA; 15759 MW; 127828 CN; SEQUENCE 113 AA; 12734 MW; 78306 CN; PRT; 120 yyygrsdkyftldywgggtsvtvss 144 IMMUNOCLOBULIN V REGION; SIGNAL. 21-JUL-1986 (REL. 01, CREATED) Query Match 60.8%; Best Local Similarity 78.2%; 49.88; Best Local Similarity 56.6%; 82; Conservative 93; Conservative STANDARD; STANDARD; (MOUSE) PIR; A02098; G2MS60 EUTHERIA; RODENTIA {1}
SEQUENCE FROM N.A. MUS MUSCULUS HV43 MOUSE RESULT 7
ID HV2G_HUMAN Query Match P01819; NON TER NON TER SIGNAL CHAIN Matches Matches В 염 g g S H K H K 음 ð ò ð ð ð ÷ JUSZCZAK E.C., MARGOLIES M.N.; BIOCHEMISTRY 22:4291-4296(1983). -!- THIS CHAIN WAS ISOLATED FROM AN ANTIARSONATE MONOCLONAL ANTIBODY OF THE IGG2A SUBCLASS. IT REPRESENTS A SECOND IDIOTYPE FAMILY 9 1 mkmftllylltvvpgilsdvqlqesgpglvkpsqsialtctvtgisittgnyrwswirqf 60 Gaps 60 PGNKLEMMGYISYSGITTYNPSLKSRISITRDTSRNQFFLQLMSVTTGDTSTYYCAR 116 61 pgnklewigyiyysaitsynpspksrttitrdtsknqfflemnsltaedtatyycar 117 61 gnklewmgyisydgsnnynpslknrisitrdtsknqfflklnsvttedtatyycar 116 EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; ä EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; IG HEAVY CHAIN V REGION (733). BY SIMILARITY. Length 117; Indels LEVY N.S., MALIPIERO U.V., LEBECQUE S.G., GEARHART P.J.; J. EXY. MED. 169:2007-2019(1989).
PIR, JTG510, HVM573.
HSSP; PO1825; 1BAR.
IMMUNOGLOBULIN V REGION; SIGNAL. 17; Mismatches 12; Score 650; DB 4; L Pred. No. 5.31e-106; 01-NOV-1990 (REL. 16, CREATED) 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE) 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE) IG HEAVY CHAIN PRECURSOR V REGION (733). LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE) 117 AA. 113 AA 117 AA; 13223 MW; 77503 CN; PRT; 21-JUL-1986 (REL. 01, LAST ANNO IG HEAVY CHAIN V REGION (36-60) MUS MUSCULUS (MOUSE). 21-JUL-1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 01, LAST SEQ) 64.9%; 74.4%; 87; Conservative STANDARD; STANDARD; 117 1115 1115 MUS MUSCULUS (MOUSE) Best Local Similarity EUTHERIA; RODENTIA. EUTHERIA; RODENTIA. SEQUENCE FROM N.A.

STRAIN=A/J; 84024551

SEQUENCE.

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9 5 60 pgkglewlgtiwgngstdynstlksrltitkdnsksqvflkmnslqtddtaryycasvsi 119 60 PGNKLEWMGYISYSGITTYNPSIKSRISITRDTSKNOFFLQINSVTTGDTSTYYCAR-SL 118 19 DVQLQESGPVLVKPSQSLSLTCTVTGYSTISDHAMSWIRQFPGNKLEMMGYISYSGITTY 78 1 mavlallfclatfpscilsqvqlkesgpglvapsqslsitctvsgfsltg-ygvnwvrqp 59 1 evqlqesqpslvkpsqtlsltcsvtgdsitsdy-wnwirkfpgnklehmgyisysgstyy 59 Gaps Gaps 81012133 SAKANO H., MAKI R., KUROSAWA Y., ROEDER W., TONEGAWA S.; NATURE 286:676-683(1980). -!- THE SEQUENCE SHOWN IS TRANSLATED FROM A DIFFERENTIATED GENE ISOLATED FROM A MYELLOMA THAT SECRETES IGG2B. PIR, A02094; G2MS14. HSSP; P01772; 1FDL. IG HEAVY CHAIN V REGION (MOPC 141). 9 EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; 6 Score 499; DB 4; Length 144; Pred. No. 3.32e-75; 30; Mismatches 24; Indels Score 609; DB 4; Length 113; Pred. No. 1.40e-97; 10; Mismatches 10; Indels

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HOMO SAPIENS (HUMAN)
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Pred. No. 1.40e-71;
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J. BIOL. CHEM. 253:585-597(1978).
-!- THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOWA PROTEIN.
PIR; A02100; G14UNM.
PDB; 7FAB; 31-JAN-94.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29; Mismatches 23;
               21-JUL-1986 (REL. 01, CREATED)
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117 AA; 12790 MW; 79791 CN;
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                                                                    IG HEAVY CHAIN V-II REGION (NEWM).
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21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN PRECIOSOR V REGION (MC101).
MUS MUSCULIOS (MOOSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; 5; EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; IG HEAVY CHAIN V REGION (PJ14) Query Match 45.4%; Score 455; DB 4; Length 115; Best Local Similarity. 57.8%; Pred. No. 2.28e-66; 23; Mismatches 24; Indels Indels SAKANO H., MAKI R., KUROSAWA Y., ROEDER W., TONEGAWA S.; NATURE 286:676-683(1980). 28; 21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-JUC-1992 (REL. 23, LAST ANNOTATION UPDATE)
IG HEANY CHAIT PRECURSOR V REGION (PJ14).
MUS MUSCULUS (MOUSE). 116 AA. Mismatches 115 AA 20 115 IG HEAVY CH 115 115 115 AA, 12447 MM, 73384 CN, PRT; PRT; 124 wndvdyyygmdvwgqgttvtvss 146 :|| ||||||||| 122 -TAMDY-----WGQGTSVTVSS 137 24; IMMUNOGLOBULIN V REGION; SIGNAL. 67; Conservative Conservative STANDARD; STANDARD; 115 115 PIR; A02095; HVMS14. HSSP; P01772; IFDL. EUTHERIA; RODENTIA. SEQUENCE FROM N.A. HV45 MOUSE P01821; 80**;** HV44 MOUSE NON TER SEQUENCE 81012133 P01820; SIGNAL CHAIN Matches Matches RESULT 셤 අ Š g õ 셤 ð 셤 δ ð

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ä 5 64 LEMMCYISYSGITTYNPSIKSRISITRDISKNOPFLQINSVTTGDISTYYCARSLARITA 123 62 lewigvvrtdgstaiadslknrvtitkdngkkqvylqmngmevkdtamyyctstlagtag 121 1 mavlgllfclvtfpscvlsqvqlkqsgpglvqpsqslsitctvsgfslts-ygvhwvrqs 59 EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA 4 ifvifmffspscilsqt-lqesgpgtvkpseslrltctvsgfeltsyyvy-wirqpprkt 61 4 LILEMIETAFPGILSDVQLQESCPVLVKPSQSLSLTCTVTGYSITSDHAMSMIRQFPGNK 63 Gaps Gaps 60 pgkglewlgviwsggstdynaafisrlsiskdnsksqvffkmnslqsndtaiyycar 116 a, 2; IG HEAVY CHAIN V REGION (MC101). IG HEAVY CHAIN V REGION (XIG8) Score 442; DB 4; Length 136; Pred. No. 8.99e-64; 33; Mismatches 35; Indels Score 442; DB 4; Length 116; Pred. No. 8.99e-64; 27; Mismatches 25; Indels MIYATA T., MORIWAKI K., HONJO IG HEAVY CHAIN PRECURSOR V REGION (XIG8) (FRAGMENT). SEQUENCE FROM N.A.
8817691 SCHWAGER J., MIKORYAK C.A., STEINER L.A.; PROC. NATL. ACAD. SCI. U.S.A. 85:2245-2249(1988). 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE) 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE) 136 AA 136 AA; 15123 MW; 110289 CN; 75942 CN; PRT; XENOPUS LAEVIS (AFRICAN CLAWED FROG) KATAOKA T., NIKAIDO T., MIYATA T. J. BIOL. CHEM. 257:277-285(1982). IMMUNOGLOBULIN V REGION; SIGNAL. IMMUNOGLOBULIN V REGION; SIGNAL. 116 AA; 12593 MW; 01-FEB-1991 (REL. 17, CREATED) Query Match 44.1%; Best Local Similarity 53.8%; Matches 63; Conservative Query Match 44.1%; Best Local Similarity 47.4%; 64; Conservative 122 yfehwgggtmvtvts 136 : ||||| |||:| STANDARD; PIR; A31933; A31933. HSSP; P01789; ZFGW. PIR; A02096; G1MS10. HSSP; P01772; 1FDL. HV01 XENLA NON TER SEQUENCE SEQUENCE Query Match NON TER NON TER SIGNAL SIGNAL CHAIN CHAIN Matches g 셤 g ò ð SO FIFFE DR RA 음 à 셤 ð

124 -MDYWGQGTSVTVSS 137

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1 <1 17 115 120 138 136	CONFLICT 75 CONFLICT 89 CONFLICT 115 CONFLICT 120 SEQUENCE 136 AA;	Query Match 42.8%; Score 429; DB 4; Length 136; Best Local Similarity 47.1%; Pred. No. 3.48e-61; Matches 64; Conservative 30; Mismatches 39; Indels 3; Gaps	Db 2 Inlvflulilkgvqcdvqlvesggglvqpggsrklscaasgftfss-fgmhwrqapekg 60	64	77	RESULT 15 ID 44V2E HUMAN STANDARD; PRT; 129 AA. AC P01824; DT 21-JUL-1986 (REL. 01, CREATED) DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) DF 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE) DE IG HEAVY CHAIN V-II REGION (WAH). OS HOMO SADIENS (HUMAN).	EUTHERIA; METAZOA; CHOKUAIA; VETHERIA; PRIMATES. [1] SEQUENCE. SEQUENCE. PROZ. 1. TETAERT D., DEBUJ PROC. NATL. ACAD. SCI. U.S.A!- THIS CHAIN WAS ISOLATED FROM PR, A02099; DEHWA. HSSP, PO1607; IECV. IMMUNOGLOBULIN V REGION. NON_TER. 129 129	2ue 3e£ 1at	Db 2 Iqlqesqpqlvkpsetlsltcivsqppirrtgywqwirqppgkglewiggvytgsiyy 61
RESULT 13 ID HV2E HUMAN STANDARD; PRT; 121 AA. AC P01818; DT 21-JUL-1986 (REL. 01, CREATED) DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE) DE 121-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE) DE 15 HEAVY CHAIN V-11 REGION (HE).				43.7%; Sco Similarity 52.1%; Pro 63; Conservative 26,	Db 1 qvilkengptlvkptetltltctlsglslttdgvavgwirggpgralewlawllywdddk 60 : : :: : : :	Db 61 rfspslksrltvtrdtsknqvvltmtnmdpvdtatyycvhrhprtlafdvwggqtkvavs 120 :: ::	RESULT 14 AC P01783 AC P01783 DT 21-JUL-1986 (REL. 01, CREATED) DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) DT 01-MOV-1990 (REL. 16, LAST ANNOTATION UPDATE) DT 01-MOV-1990 (REL. 16, LAST ANNOTATION (MOPC 21) (FRAGMENT). SE IG HEAVY CHAIN PRECURSOR V REGION (MOPC 21) (FRAGMENT). SE WIS MUSCULUS (MOUSE). CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		RL CELL 24:625-63/(1981). RN [2] RP SEQUENCE OF 17-136. RM 77100368 RA ADETUGBO K., MILSTEIN C., SECHER D.S.; RL NATURE 265:299-304(1977). DR HSSP; PO1607; JFGV. KW HWMNOGLOBULIN V REGION; SIGNAL.

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protein - protein database search, using Smith-Waterman algorithm MPerch_pp

Mon Jul 8 08:34:49 1996, MasPar time 4.28 Seconds 265.081 Million cell updates/sec Run on:

Tabular output not generated.

Description: Perfect Score:

>US-08-137-117B-31 (1-137) from USO8137117B.pep 1002 1 MRVLILIMLFTAFPGILSDV......LARTTAMDYWGQCTSVTVSS 137 Sequence:

PAM 150 Gap 11 Scoring table:

70887 seqs, 8282111 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq22
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14

Mean 30.530; Variance 155.534; scale 0.196 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	6.61e-72	8.43e-51	8.43e-51	4.52e-49	1.16e-48	2.91e-47	8.77e-46	5.60e-44	5.60e-44	2.54e-43	5.76e-40	1.22e-39
Description	pPM-h1 protein produc	puc-RVh-PM1f-4.	puc-RVh-PM1f.	Fv (TU27).	MaE13 heavy chain.	Sequence encoded by t	Sequence of a chimeri	Sequence of the monoc	VH domain of antibody	Heavy chain of 58.2 a	MaEll heavy chain.	HYH heavy chain.
ID	R28671	R29014	R29012	R34510	R33308	R24722	R24721	R48617	R07318	R63118	R33306	R38608
DB	و	9	9	-	9	S	S	6	7	12	9	-
% Query Aatch Length DB	137	138	138	240	130	126	122	114	117	225	134	113
% Query Match	100.0	74.6	74.6	72.5	72.0	70.3	68.5	66.3	66.3	65.5	61.4	61.0
Score	1002	747	747	726	721	704	989	664	664	959	615	611
Result No.	1	7	m	4	S	9	7	œ	ð	10	Π	12

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120 10 R54929
144 1 P80892
42 2 R06

ALI GNMENTS

pPM-hi protein product.

Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H; heavy chain; variable region; mouse; monoclonal; hybridoma; PMI; plasmid; pPM-k3; pPM-h1. Reconstituted human antibody to human interleukin-6 receptor has low antigenicity and contains mouse V-region complementarity determining regions
Disclosure, Page 122-123, 207pp; Japanese. Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M; WPI; 92-398882/48. N-PSDB; Q30756. Location/Qualifiers R28671 standard; Protein; 137 AA. 30-MAR-1993 (first entry) (CHUS) CHUGAI SEIYAKU KK. Protein 19.137 /note= "Mature peptide" W09219759-A. /note= "Signal peptide" 24-APR-1992; J00544. 25-APR-1991; JP-095476. 19-FEB-1992; JP-032084. 12-NOV-1992 Synthetic. Key Peptide R28671;

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/note= Region Region Region Region Region Region 88888888 셤 ð a ð 음 ð ö The sequences given in R28670-71 were encoded by plasmids which were used in example to illustrate the production of a human antibody which recognises human interleukin-6 receptor (IL-6R). The antibody comprises light (L) chain and heavy (H) chain variable regions which were derived from a mouse monoclonal antibody produced from the hybridoma PMI which contained the plasmids pPM-K3 and pPM-H1. gnklewmgyisysgittynpslksrisitrdtsknqfflqlnsvttgdtstyycarslar 120 1 mrvlillwlftafpgilsdvqlqesgpvlvkpsqslsltctvtgysitsdhawswirqfp 60 1 MRVLILLMLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFP 60 Gaps complementarity determining region; mouse; monoclonal; hybridoma; has low antigenicity and contains mouse V-region complementarity ; 0 Reconstituted human antibody to human interleukin-6 receptor Score 1002; DB 6; Length 137; Pred. No. 6.61e-72; Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR; 0; Indels Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M; WPI; 92-398882/48. plasmid; polymerase chain reaction; amplify. 0; Mismatches Disclosure; Page 142-3; 207pp; Japanese. Location/Qualifiers JT 2 R29014 standard; Protein; 138 AA. Query Match 100.0%; Best Local Similarity 100.0%; Matches 137; Conservative 121 TTAMDYWGQGTSVTVSS 137 121 ttamdywgqgtsvtvss 137 30-MAR-1993 (first entry) (CHUS) CHUGAI SEIYAKU KK 128..138 118..127 peptide" 24-APR-1992; J00544. 25-APR-1991; JP-095476. 19-FEB-1992; JP-032084. 86..117 20..49 50..55 70..85 56..69 determining regions puc-RVh-PM1f-4. "Leader N-PSDB; Q31365 Region /label= FR3 'label= CDR3 /label= CDR2 /label= CDR1 label= FR2 W09219759-A 12-NOV-1992 /label= FR1 /label= FR4 Synthetic. Sequence R29014; Peptide /note= Region Region Region Region Region Region 19 ន្តខន្ធន្តន្ត 셤 õ 셤 쇰 8 ACCAMENTAL DATE OF THE STATE OF δ

ö The sequences given in R29012-15 are portions of monoclonal antobodies which were encoded by plasmids derived from mouse hybridomas. The DNA encoding complementarity determining regions (CDK's) was isolated by polymerase chain reaction. These antibodies recognise human interleukin-6 receptor (IL-6R). The mouse hybridoma cells were 66 ewigyisysgittynpslksrvtmlrdtskngfslrlssvtaadtavyycarslarttam 125 65 EMMCYISYSGITTYNPSIKSRISITRDTSKNQFFLQLNSVTTGDTSTYCARSLARTTAM 124 65 64 Gaps transformed with the plasmids encoding these genes which caused the secretion of these antibodies from the hybridoma cells. 6 iilfluatatgvhsgvqlqesgpglvrpsqtlsltctvsgysitsdhawswvrgppgrgl 5 ILLMLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKL complementarity determining region; mouse; monoclonal; hybridoma; has low antigenicity and contains mouse V-region complementarity determining regions ; 0 Reconstituted human antibody to human interleukin-6 receptor Score 747; DB 6; Length 138; Pred. No. 8.43e-51; Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR; 19; Mismatches 13; Indels Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M; plasmid; polymerase chain reaction; amplify. Location/Qualifiers R29012 standard; Protein; 138 AA. Query Match 74.6%; Best Local Similarity 75.9%; Matches 101; Conservative 30-MAR-1993 (first entry) (CHUS) CHUGAI SEIYAKU KK. 128..138 118..127 86..117 25-APR-1991; JP-095476. 20..49 50..55 70..85 19-FEB-1992; JP-032084 126 dywgqgslvtvss 138 125 DYWGQGTSVTVSS 137 24-APR-1992; J00544. WPI; 92-398882/48. 138 AA; N-PSDB; Q31360 DUC-RVh-PM1f. /label= CDR2 'label= CDR3 /label= CDR1 Region /label= FR3 W09219759-A 'label= FR4 12-NOV-1992 /label= FR1 /label= FR2 Synthetic. Sequence Peptide

Disclosure;

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Sequence encoded by the anti-urokinase antibody kappa variable region

R24722 standard; Protein; 126 AA

28-DEC-1992 (first entry)

(VK) CDNA

Chimeric monoclonal antibody; anti-urokinase antibody; PCR;

antithrombotic agent; myocardial infarction therapy

Location/Qualifiers

Mus musculus.

/label= complementarity determining region(CDR)1

/label= CDR 2

Region

34..39

Region

ö closure; Page 138-9; 207pp; Japanese. sequences given in R29012-15 are portions of monoclonal antobodies The DNA 66 ewigyisysgittynpslkørvtmlrdtsknqfslrlssvtaadtavyycarslarttam 125 9 encoding complementarity determining regions (CDR's) was isolated by 5 ILLMLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKL 64 The constructed plasmids prv(TU27)-DE and prv(TU25)-DE which express Gaps inflammatory allergic and autoimmune diseases, or leukemia. Unlike transformed with the plasmids encoding these genes which caused the secretion of these antibodies from the hybridoma cells. chain of IL-2 receptor and of inhibiting the binding of IL-2 to the 6 iilflvatatgvhsqvqlqesgpglvrpsqtlsltctvsgysitsdhawswvrqppgrgl sequenced. The polypeptides are capable of binding to the beta polypeptides consisting only of the V regions were purified and interleukin-6 receptor (IL-6R). The mouse hybridoma cells were Polypeptide(s) which bind H chain of human IL-2 receptors - for immunosuppressants, e.g. to prevent graft rejection or to treat which were encoded by plasmids derived from mouse hybridomas. ö heavy; beta; chain; interleukin; IL-2; receptor; inhibition; immunomodulator; immunosuppressant; graft rejection; allergy; polymerase chain reaction. These antibodies recognise human treating inflammatory, allergic and auto-immune disorders, Length 138; 19; Mismatches 13; Indels pFv(TU27)-DE; pFv(TU25)-DE; V region; antibody; binding; receptor. They are useful as immunomodulators and cyclosporin etc. they are both effective and safe Score 747; DB 6; 1 Pred. No. 8.43e-51; autoimmune disease; leukemia; cyclosporin. .r 4 R34510 standard; Protein; 240 AA. Taki S; Claim 3; Page 18; 27pp; English. Query Match 74.6%; Best Local Similarity 75.9%; 101; Conservative 20-AUG-1993 (first entry) 30-SEP-1992; 116746. 03-OCT-1991; JP-256335. Hamuro J, Shimamura T, 126 dywgqgslvtvss 138 |||||||: ||||| | 125 DYWGQGTSVTVSS 137 (AJIN) AJINOMOTO KK. WPI; 93-145163/18. 240 AA; leukaemias etc. N-PSDB; Q40462 Homo sapiens. EP-539748-A. 05-MAY-1993. Sequence Sequence Fv (TU27) Matches g ð 요 음

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77 18 SDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAMSWIRQFPGNKLEMMGYISYSGITT à

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8 19 DVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEMMCYISYSGITTY 78 61 npslksrisitrdtsknqfflqlnsvttedtatyycawvva--yamdywgqgtsvtvss 117 79 NPSIKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLARTTAMDYWGQGTSVTVSS 137 Gaps analogous residue from a Kabat CDR domain of the murine anti-hulgE antibodies MAE11, MAE13, MAE15 or MAE17. 1 dvqlqesqpqlvipsqslsltctvtgytitsdnawnwirqfpgnklewmgyinhsgttsy Polypeptide(s) binding to specific Fc epsilon receptors - act as IgE antagonists; useful for treating and preventing IgE-mediated disorders e.g. allergies histamine release from mast cells or basophils, comprise a human Kabat CDR domain into which has been substituted a positionally 2; Disclosure, Fig 2, 113pp, English. Antibodies capable of binding FCEL-bound IgE but which are substantially incapable of binding FCEH-bound IgE or inducing Score 721; DB 6; Length 130; Pred. No. 1.16e-48; 7; Indels receptor; histamine; mast cell; basophil; Kabat; murine; MAE11; MAE13; MAE15; MAE17. Antibody; high affinity; FCEH; low affinity; FCEL; IgE receptor; histamine; mast cell; basophil; Kaha 8; Mismatches .r 5 R33308 standard; protein; 130 AA. / Match 72.0%; Local Similarity 85.7%; 05-JUL-1993 (first entry) 102; Conservative 07-MAY-1992; US-879495. Jardieu PM, Presta LG; 14-AUG-1991; US-744768. (GETH) GENENTECH INC. 14-AUG-1992; U06860. 130 AA; MaE13 heavy chain. WPI; 93-094004/11 WO9304173-A. 04-MAR-1993 Synthetic. Sequence Query Match R33308; Matches DATE OF THE PART O 셤 ð g ð

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WPI; g 쇰 ð 셤 ò ð 2; 64 npslksrisitrdtsnnqfflqlnsvtsedtatyycarlgdfdagdyfdywggyttvtvs 123 79 NPSLKSRISITRDTSKNOFFLQLNSVTTGDTSTYYCAR-S-LARTTAMDYWGQGTSVTVS 136 4 evqlvesgpglvkpsgslsltctvtgysitsdyawnwirqfpgnklewmgyinysgttsy 63 Gaps antibody-producing hybridoma UK1-3 cells. Using this poly (A) RNA as a template, an anti-urokinase antibody VK cDNA was amplified with the mC-Kappa primer as primer for first strand sysnthesis, and the 3'mV-kappa and 5'mV-kappa primers as primers for the PCR. The amplified fragment was restriction digested and ligated into a restriction fragment of pTB1423 to give an anti-urokinase antibody VK cDNA contg. plasmid pTB1456. The sequence of this plasmid is given in Q2567. The cDNA is a functional VK gene. The sequence of Sequence of a chimeric urokinase-recognising antibody heavy chain variable region contg. complementarity determining regions (CDRs) antibody light and heavy chain variable and constant for treating 5; Chimeric monoclonal antibodies - contain anti-human fibrin Score 704; DB 5; Length 126; Pred. No. 2.91e-47; 10; Mismatches 11; Indels Chimeric monoclonal antibody; anti-urokinase antibody; antithrombotic agent; myocardial infarction therapy Poly(A) + RNA was prepd. from mouse anti-urokinase thrombotic conditions e.g. myocardial infarction Example; Figure 15; 87pp; English. the primer (mC-gamma-1) is given in Q25689. Iwasa S, Taka H, Watanabe T, Tada H; Location/Qualifiers R24721 standard; Protein; 122 AA. (TAKE) TAKEDA CHEM IND LTD. Query Match 70.3%; Best Local Similarity 81.0%; 98; Conservative 28-DEC-1992 (first entry) 102..113 99..110 11-NOV-1991; JP-294464. 51..66 18-DEC-1990; JP-413829. 31..36 17-DEC-1991; 121591. 17-DEC-1991; 121591. WPI; 92-209528/26. N-PSDP; Q25667. /label= CDR J /label= CDR K /label= CDR L /label= CDR 3 EP-491351-A EP-491351-A 24-JUN-1992 24-JUN-1992 J, K and L. 124 s 124 137 S 137 Synthetic. Sequence Region Region Region Matches RESULT 셤 δ 셤 ð 음 ð

urokinase-recognising antibody heavy chain variable region contg. at least one of the polypeptide chains J, K and L (R24717,R24718,R24719) and a human antibody heavy chain constant region. A prefd. chimeric monoclonal antibody contains all three complementarity determining The inventors claim a chimeric monoclonal antibody which contains a and, since they have very low immunogenicity as compared with mouse Abs, they can be administered to humans for diagnostic and therapeutic purposes. They are also more stable and show a longer antibody light and heavy chain variable and constant for treating regions. The chimeric Abs can be used both in vivo and in vitro half-life in the blood as compared with the original mouse Abs Chimeric monoclonal antibodies - contain anti-human fibrin thrombotic conditions e.g. myocardial infarction Disclosure; Page 10; 87pp; English. Iwasa S, Taka H, Watanabe T, Tada H; WPI; 92-209528/26. (TAKE) TAKEDA CHEM IND LTD. 11-NOV-1991; JP-294464 Sequence

60 npslksrisitrdtsnnqfflqlnsvtsedtatyycarlgdfdagdyfdywgqgttvtvs 119 79 NPSIKSRISITRDISKNOFFLOIMSVITGDISTYYCAR-S-LARITAMDYWGQGISVIVS 136 59 Gaps 19 DVQLQESGPVLVKPSQSLSLTCTVTGYSTTSDHAWSWIRQFPGNKLEMMCYISYSGITTY 1 evqlvesgpglvkpsqslsltctvtgysitsdyawnw-rqfpgnklewmgyinysgttsy 3; Score 686; DB 5; Length 122; Pred. No. 8.77e-46; 10; Mismatches 11; Indels Query Match 68.5%; Best Local Similarity 80.2%; 97; Conservative Query Match Matches

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Sequence of the monoclonal antibody BAT123 heavy chain Epitope; monoclonal antibody; BAT123; variable heavy. R48617 standard; Protein; 114 AA. 03-SEP-1994 (first entry) variable region. Synthetic. R48617;

(NISP) NISSIN SHOKUHIN KAISHA LTD. 24-AUG-1992; WO-U07111. 22-APR-1993; US-039457. 24-AUG-1993; U07967. 94-083117/10 WO9404574-A. 03-MAR-1994 Ohno T;

Example: Page 46-47; 91pp; English. GPGR is a portion of HIV-1 gp120 or gp160 protein. Monoclonal antibodies (MAbs) that react with this and which have the capacity to neutralise the infection of H9 cells in culture by live HIV-1 strains MN and IIIB are claimed. Specifically illustrating the New humanised antibody specific for epitope on HIV-1 gp 120 -able to neutralise infection of HG cells, also nucleic acid encoding it, useful for passive immunisation to treat or prevent HIV-1 infection

invention are the murine MAb (designated NM-01) produced by

10180824

10726. The DNA sequences of the variable regions of the heavy and light chains of MAb NM-01 were cloned by PCR using cDNA generated

from hybridoma HB 10726 cytoplasmic RNA as template. The DNA was then sequenced. The DNA and deduced AA sequences are given in

888888888888888888888

114 AA;

Sequence

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compared to NM-01

cell line HB 10726 which is deposited under ATCC No. HB

22 LQESGPVLVKPSQSLSLTCTVTGYSITSDHAMSWIRQFPGNKLEWMGYISYSGITTYNPS

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Location/Qualifiers /note= "CPR no further definition' further definition 'note= "CPR no further definition" R33306 standard; protein; 134 AA. R63118 standard; peptide; 225 AA. Query Match 65.5%; Best Local Similarity 78.6%; 99; Conservative (SCRI) SCRIPPS RES INST. 05-JUL-1993 (first entry) 09-FEB-1994; U01458. 12-FEB-1993; US-017485. (REPK) REPLIGEN CORP. Profy AT, Wilson IA; 160 162 201 WPI; 94-332662/41. 121 tvtvss 126 132 SVTVSS 137 /note= "CPR no OTHER Modified site Modified site Modified site Homo sapiens. /label= OTHER /label= OTHER W09418232-A 18-AUG-1994 Sequence /label= R33306; R63118; Matches RESULT ID R3 g 셤 염 ð à ð Ξ. 3; 61 npslksrisitrdtsknlfflqlssvtsedtatyycarg---sfg-d-wgqgtlvtvsa 114 1 lqesqpdlvkpsqslsltctvtgysitsgyswhwirqfpgnklewmgyiqysgitnynps 60 1 evqlqesgpglvkpsqslsltctvtgysitsdyawnwirqfpgnklewmgyisysgstty 60 79 NPSIKSRISITRDISKNQFFLQINSVITGDISTYYCARSIARTTAMDYWGQGISVIVSS 137 Gaps 3; Mismatches 17; Indels 1; Gaps Antibody B is produced as described in EP-141079 and binds to cells Q5685/R48613, Q56886/R48615. Resequencing the variable regions of MAD NM-01 resulted in the sequences set out in Q5687/R48614 and Q5688/R48616. The heavy chain variable region of NM-01 differs from that of the MAD BA123, as reported in Liou et al., by 46 AAs out of a total of 120. The light chain variable regions of these two Abs differ by 23 AAs. Significantly, the three CDRs in the heavy chain (V-H) of the NM-01 molecule are about 41 to 90% different in sequence from those of BAT123, while the sequences of They are useful in tumour diagnosis and therapy. See also Q06215 for VK of MAb B, Q07312-13 for MAb A and Q06227-30 5; Monoclonal antibodies to tumour associated antigens - used for the three CDRs in the light chain (V-L) vary by about 29-47% gastrointestinal carcinoma; ovary; pulmonary adenocarcinoma; VH domain of antibody B against tumour-associated antigens. Tumour-associated antigen; murine monoclonal antibody B; almost all gastrointestinal carcinomas and to certain ovary Score 664; DB 9; Length 114; Pred. No. 5.60e-44; 9; Mismatches 7; Indels Score 664; DB 2; Length 117; Pred. No. 5.60e-44; carcinomas and pulmonary adenocarcinomas diagnosis of malignant tumours etc. (BEHW) BEHRINGWERKE AG. Bosslet K, Seemann G, Sedlacek HH; WPI; 90-291873/39. Disclosure; Page 12; 18pp; German .r 9 R07318 standard; protein; 117 AA. Query Match 66.3%; Best Local Similarity 82.4%; Matches 98; Conservative Query Match 66.3%; Best Local Similarity 82.1%; 22-JAN-1991 (first entry) 96; Conservative 21-MAR-1990; 105322. 24-MAR-1989; DE-909799.

for MAb C and D.

Sequence

Matches

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N-PSDB; Q07318

RESULT

Mus musculus. EP-388914-A. 26-SEP-1990

diagnosis.

R07318;

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ä 61 npslksrisitrdtsknqfflqlnsvttedtatyycareeampygnqayyyamdcwqqqt 120 79 NPSLKSRISITRDTSKNOFFLQLNSVTTGDTSTYYCAR--SLA---RTT--AMDYWGQGT 131 19 DVQLQESGPVLVKPSQSLSLTCTVTCXSITSDHAMSWIRQFPGNKLERMCYISYSGITTY 78 7; Gaps 92 IKSRISITRDISKNOFFLOINSVITGDISTYCAR-SLARITAMDYNCQGISVIVSS 137 61 lksrisitrdtsknqfflqlnsvttedtatyycaredydyhwyfdvwgagttvtvss 117 1 dvqlqqsqpdlvkpsqslsltctvtgysitsgyswhwirqfpgnklewmgyihysagtny Identifying cpds. which elicit, or bind to, anti-HIV antibodies — and new antibodies which neutralise a broad range of HIV strains Disclosure; Page 50; 137pp; English. R63118 describes the amino acid sequence of the heavy chain of 58.2 an anti-HIV antibody (Ab), it was used in the development of the peptide AS (R63119). This peptide can bind to anti-HIV Abs or elicit new Abs effective against a broad range of HIV strains, Score 656; DB 12; Length 225; Pred. No. 2.54e-43; 26-JUN-1995 (first entry)
Heavy chain of 58.2 an anti-HIV antibody.
Identifying compounds; anti-HIV antibodies; HIV treatment; peptide AS; antibody 58.2. 10; Mismatches 10; Indels that can be used in the treatment of HIV infection g ð ð

95; Conservative 07-MAY-1992; US-879495. (GETH) GENENTECH INC. Jardieu PM, Presta LG; 137 AA; Synthetic. WO9304173-A. 04-MAR-1993. Sequence Sequence Query Match Matches Matches q δ a 임 용 88888888888888 δ δ ñ The amino acid sequences of the light and heavy chains of the variable domains from antibodies HYH [HYHEL-10 Fab-lysosyme complex] (R38601 and R38608, respectively), MCPC [IgA Fab MCPC603-phosphocholine 61 npslknrisvtrdtsqnqfflklnsataedtatyycarg-shyfghwhfavwgagttvtv 119 79 NPSIKSRISITRDTSKNGFFLQLMSVTTGDTSTYYCARSLARTTAM-DY--WGQGTSVTV 135 19 DVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAMSWIRQFPGNKLEMMGYISYSGITTY 78 1 dvqlqesgpglvkpsqslslacsvtgysitsgyswnwirqfpgnklewmgsitydgssny 60 4; Gaps analogous residue from a Kabat CDR domain of the murine anti-hulgE antibodies MAE11, MAE13, MAE15 or MAE17. ا م histamine release from mast cells or basophils, comprise a human Kabat CDR domain into which has been substituted a positionally Polypeptide(s) binding to specific Fc epsilon receptors - act as IgE antagonists; useful for treating and preventing IgE-mediated substantially incapable of binding FCEH-bound IgE or inducing Antibodies prepn. used for treatment of auto-immune diseases replacement of critical residues to reduce immunogenicity but affinity; antigen; immunogenicity; humanisation; framework. Disclosure; Fig 2; 113pp; English. Antibodies capable of binding FCEL-bound IgE but which are Query Match 61.4%; Score 615; DB 6; Length 134; Best Local Similarity 70.5%; Pred. No. 5.76e-40; 16; Mismatches 16; Indels HYH heavy chain. Antibody; variable domain; light; L; heavy; H; consensus; IgE receptor; histamine; mast cell; basophil; Kabat; CDR; murine; MAE11; MAE13; MAE17; MAE17 Antibody; high affinity; FCEH; low affinity; FCEL; Kohn FR, Little RG, Studnicka GM; retain binding affinity, etc. Disclosure; Page 87-88; 160pp; English. R38608 standard; peptide; 113 AA. 86; Conservative 28-0CT-1993 (first entry) W09304173-A. 04-MAR-1993. 14-AUG-1992; U06860. 14-AUG-1991; US-744768. 07-MAY-1992; US-879495. disorders e.g. allergies 13-DEC-1991; US-808464. Presta LG; (GETH) GENENTECH INC. 14-DEC-1992; U10906 Fishwild DM, Kohn WPI; 93-213827/26. (XOMA) XOMA CORP. 134 AA; chain. WPI; 93-094004/11 Homo sapiens WO9311794-A. MaE11 heavy Jardieu PM, 24-JUN-1993 120 ss 121 136 SS 137 Sequence R38608; Matches

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3 complex] (R38602-03 and R38609-10, respectively), NEWN [Ig Fab' NEW] (R38604-05 and R38611, respectively) and KOL [IgG1 KOL] (R38606-07 and R38612, respectively) may be used to determine an alignment from which replacement of entire antibody framework regions with those of human antibodies, this method involves only the introduction of human 6; Gaps This ensures that the binding properties of the modified antibody residues into those positions not critical for antigen binding. Score 611; DB 7; Length 113; Pred. No. 1.22e-39; 9; Indels appropriate changes may be made. Unlike other methods of humanisation, which advocate the 12; Mismatches 61,0%; Best Local Similarity 77.3%; 92; Conservative are not diminished. 113 AA;

R33310 standard; Protein; 137 AA.

IgE receptor; histamine; mast cell; basophil; Kabat; Antibody; high affinity; FCEH; low affinity; FCEL; CDR; murine; MAE11; MAE13; MAE15; MAE17 05-JUL-1993 (first entry) MaE15 heavy chain.

14-AUG-1991; US-744768. 14-AUG-1992; U06860.

Polypeptide(s) binding to specific Fc epsilon receptors - act as IgE antagonists; useful for treating and preventing IgE-mediated WPI; 93-094004/11.

disorders e.g. allergies

Disclosure; Fig 2; 113pp; English.
Antibodies capable of binding FCEL-bound IgE but which are substantially incapable of binding FCER-bound IgE or inducing histamine release from mast cells or basophils, comprise a human Kabat CDR domain into which has been substituted a positionally analogous residue from a Kabat CDR domain of the murine anti-hulgE antibodies MAEI1, MAEI3, MAEI5 or MAEI7.

5 Length 137; 5; Mismatches 19; Indels Score 606; DB 6; Pred. No. 3.13e-39; Query Match Best Local Similarity 76.6%;

5;

Gaps

61 npslkrrisitddtsknqfflqlnsvttedtatyycargsiyyygsryryfdvwgagttv 120

= = =

79 NPSLKSRISITRDISKNQFFLQLNSVTTGDTSTYYCAR-SL---ARTTAMDYWGQGTSV 133

ð

Biosynthetic antibody binding site. Biosynthetic antibody binding site; framework region; assay; imaging;

multifunctional protein.

WO8809344-A. 01-DEC-1988

US-08-137-117B-31.rag

Carcinoembryonic antigen; single chain variable region; 8Fv fragment; fusion gene; cancer treatment; targetted drug delivery; tumour. useful for targetting beta-glucuronidase to cancer cells expressing internalisation via the mannose-6-phosphate and qalactose receptors CEA, where the enzyme is able to convert a prodrug into its active form. Any fusion protein not bound to tumour can be removed by The sequence R50092 comprises a humanised sFv-fragment against CEA fused to a human beta-glucuronidase. The fusion protein is New fusion protein contg. enzyme for prodrug activation - coupled to antigen binding component, esp. sFv antibody fragment, partic. 26-OCT-1994 (first entry)
Humanised anti-CEA sFv fragment-human beta-glucuronidase fusion Score 596; DB 10; Length 909; Pred. No. 2.06-38; /note= "humanised anti-CEA sFv fragment fused to Bosslet K, Czech J, Gehrmann M, Seemann G; WPI; 94-111012/14. Location/Qualifiers Claim 13; Page 12-15; 35pp; German. .T 14 R50092 standard; Protein; 909 AA. Best Local Similarity 61.9%; Matches 83: Corre human beta-glucuronidase for treatment of tumours /label= signal_peptide Protein 20..909 (BEHW) BEHRINGWERKE AG /label= fusion_protein 02-0CT-1992; DE-233152 24-SEP-1993; 115418 909 AA: N-PSDB; Q58896. Homo sapiens. 121 tvss 124 134 TVSS 137 06-APR-1994 EP-590530-A Sequence Protein protein. Peptide 셤 ð

Disclosure; 15pp; English.
The biosynthetic antibody binding site (BABS) forms part of a recombinant multifunctional protein which also comprises an effector protein, an AA sequence capable of sequestering an ion, or a sequence capable of binding to a solid support. The BABS comprises framework regions and

Recombinant multifunctional protein - having antibody binding site and sequence for biological activity, ion sequestering or binding to a

(CREA-) Creative Biomolecules Inc.

Oppermann H;

Huston JS,

WPI; 88-353928/49

solid support.

MARKER MA

21-MAY-1987; US-052800.

19-MAY-1988; U01737.

specificity. The effector protein is an enzyme, toxin, receptor, binding site, growth factor, lymphokine, cytokine or antimetabolite. The sequence

complementarity determining regions from MOPC-315 having dinitrophenol

capable of sequestering an ion is calmodulin or metallothionein. The sequence capable of binding to a solid support is streptavidin or a

protein A fragment. The protein may be used for, eg specific binding

assays, affinity purificn, biocatalysts, drug targetting, imaging and immunological treatment of oncogenic and infectious diseases. The protein

offers fewer cleavage sites to circulating proteolytic enzymes and have improved stability. They reach target organs rapidly and are cleared quickly from the body. They also have reduced immunogenicity.

Sequence

60 gnpslknrvsitrdtsenqfflkldsvtt---atyycagdndhlyyfdywgqgttltvsg 116 79 -NPSIKSRISITRDTSKNQFFIQINSVTTGDTSTYYCARSLARTTAMDYWGQGTSVTVSS 137 1 dvqlqesgpglvkpsqslsltcsvtgysitsgyfwnwirgfpgnklewlgfikydg-sny 59 19 DVQLQESGPVLVKPSQSLSLTCTVTGYSTTSDHAMSWIRQFPGNKLEMMGY1SYSGITTY 78 Gaps 13; Mismatches 17; Indels 5; Score 589; DB 1; Length 240; Pred. No. 7.66e-38; = Query Match 58.8%; Best Local Similarity 70.8%; 85; Conservative Matches 염 g δ ð

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Search completed: Mon Jul 8 08:35:17 1996 Job time : 28 secs.

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23; Mismatches 27; Indels 1; Gaps

126 fdvwgqgttvtvss 139

6 iilflvatatgvhsqvqlqesgpglvrpsqtlsltctvsgftissgyswhwvrqppgrgl 65

쇰 à 요 δ පු õ

5 ILLMLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKL 64

FILE 'USPAT' ENTERED AT 10:35:38 ON 03 JUL 96

=> s human interleukin 6 receptor?

133546 HUMAN

2317 INTERLEUKIN

1835874 6

23249 RECEPTOR?

L1 3 HUMAN INTERLEUKIN 6 RECEPTOR?

(HUMAN (W) INTERLEUKIN (W) 6 (W) RECEPTOR?)

=> d 1-3 bib ab clm

US PAT NO: 5,447,851 [IMAGE AVAILABLE] L1: 1 of 3

DATE ISSUED: Sep. 5, 1995

TITLE: DNA encoding a chimeric polypeptide comprising the

extracellular domain of TNF receptor fused to IgG,

vectors, and host cells

INVENTOR: Bruce A. Beutler, Dallas, TX

Karsten Peppel, Dallas, TX
David F. Crawford, Irving, TX

ASSIGNEE: Board of Regents, The University of Texas System, Austin,

TX (U.S. corp.)

APPL-NO: 07/862,495 DATE FILED: Apr. 2, 1992

ART-UNIT: 182

PRIM-EXMR: Garnette D. Draper
ASST-EXMR: K. Cochrane Carlson
LEGAL-REP: Arnold, White & Durkee

US PAT NO: 5,447,851 [IMAGE AVAILABLE] L1: 1 of 3

ABSTRACT:

The invention relates generally to DNA sequences encoding chimeric polypeptides comprising extracellular portions of cytokine receptor polypeptides attached to a sequence encoding portions of IgG polypeptides. The invention relates generally, as well, to DNA sequences encoding chimeric polypeptides comprising extracellular portions of cytokine receptor polypeptides attached through oligomers encoding specifically cleavable peptide linkers to a sequence encoding portions of IgG heavy chain polypeptides More specifically, the invention relates to a construction in which a cDNA sequence encoding the extracellular domain of the human 55 kD TNF receptor is attached through an oligomer encoding a thrombin-sensitive peptide linker to a sequence encoding the F.sub.c portion and hinge region of a mouse IgGl heavy chain. The invention relates as well to uses of the chimeric polypeptide, including: use as a reagent for the antagonism and assay of TNF and lymphotoxin from diverse species; use as a means of determining the mechanism by which TNF, or analogs thereof, interacts with the TNF receptor; use as an antitumor reagent, particularly against placental tumors; and, use as a reagent capable of controlling birth.

CLAIMS:

CLMS(1)

What is claimed is:

1. An isolated DNA segment having a sequence encoding a chimeric polypeptide comprising the extracellular domain of a TNF receptor polypeptide functionally attached to a Fc portion and hinge region of an IgG heavy chain polypeptide.

CLMS(2)

2. The isolated DNA segment of claim 1, where the TNF receptor polypeptide is a human TNF receptor polypeptide.

CLMS(3)

3. The isolated DNA segment of claim 1, where the IgG heavy chain polypeptide is a mouse IgG polypeptide.

CLMS(4)

4. The isolated DNA segment of claim 1, further incorporating a DNA segment encoding a specifically cleavable linker peptide functionally interposed between the TNF receptor polypeptide and the Fc portion.

CLMS(5)

5. The isolated DNA segment of claim 4, where the specifically cleavable linker peptide comprises a thrombin-sensitive linker peptide.

CLMS(6)

6. A recombinant vector incorporating a DNA segment as defined by claim 1.

CLMS(7)

7. The recombinant vector of claim 6, where the TNF receptor polypeptide is a human TNF receptor polypeptide.

CLMS(8)

8. The vector of claim 6, where the IgG heavy chain polypeptide is a mouse IgG polypeptide.

CLMS (9)

9. The vector of claim 6, further incorporating a specifically cleavable linker peptide functionally interposed between the extracellular domain of the TNF receptor polypeptide and the Fc portion.

CLMS (10)

10. The vector of claim 9, where the specifically cleavable linker peptide comprises a thrombin-sensitive linker peptide.

CLMS (11)

11. The vector of claim 6, where the chimeric polypeptide encoding sequence is positioned adjacent to and under the control of an effective promoter.

CLMS (12)

12. The vector of claim 11, where the promoter comprises a prokaryotic promoter, the vector being adapted for expression in a prokaryotic host.

CLMS (13)

13. The vector of claim 11, where the promoter comprises a eukaryotic promoter, the vector being adapted for expression in a eukaryotic host, and the vector further includes a polyadenylation signal position 3' of the carboxy-terminal amino acid, and within a transcriptional unit of the encoding polypeptide.

CLMS (14)

14. The vector of claim 13, where the eukaryotic promoter comprises a cytomegalovirus promoter.

CLMS (15)

15. The recombinant host cell which incorporated an isolated DNA segment in accordance with claim 1.

CLMS (16)

16. The recombinent host cell of claim 15, further defined as a eukaryotic host cell.

CLMS (17)

17. The recombinant host cell of claim 16, further defined as a CHO cell.

CLMS (18)

18. The recombinant host cell of claim 15, further defined as a prokaryotic host cell.

CLMS (19)

19. The recombinant host cells of claim 15 where the DNA segment encoding a chimeric polypeptide is under the transcriptional control of regulatory signals functional in the recombinant host cell which regulatory signals appropriately control the expression of the chimeric polypeptide in a manner to allow all necessary transcriptional and post transcriptional modification.

CLMS (20)

20. A method of producing a chimeric polypeptide comprising the extracellular domain of the TNF receptor polypeptide functionally attached to a Fc portion and hinge region of an IgG heavy chain polypeptide, the method comprising:

(a) producing a recombinant host cell according to claim 5, such cell

being capable of expressing the polypeptide;

- (b) culturing the host cell under conditions appropriate for expressing the polypeptide; and
- (c) recovering the chimetic polypeptide.

CLMS (21)

- 21. The method of claim 20, where additional steps comprise:
- (a) cleaving the polypeptide at the specifically cleavable linker peptide; and
- (b) recovering the polypeptide comprising an extracellular domain of the TNF receptor polypeptide.

CLMS (22)

22. The method of claim 20 wherein the host cell is a eukaryotic cell.

CLMS (23)

23. The method of claim 22 wherein the eukaryotic cell is a CHO cell.

CLMS (24)

24. The method of claim 22 wherein the eukaryotic cell is an insect cell.

CLMS (25)

25. The method of claim 20 wherein the host cell is a prokaryotic cell.

US PAT NO: 5,426,177 [IMAGE AVAILABLE] L1: 2 of 3

DATE ISSUED: Jun. 20, 1995

TITLE: Ciliary neurotrophic factor receptor

INVENTOR: Samuel Davis, New York, NY

Stephen P. Squinto, Irvington, NY

Mark E. Furth, Pelham, NY

George D. Yancopoulos, Briarcliff Manor, NY

ASSIGNEE: Regeneron Pharmaceuticals, Inc., Tarrytown, NY (U.S.

corp.)

APPL-NO: 07/676,647 DATE FILED: Mar. 28, 1991

ART-UNIT: 182

PRIM-EXMR: Robert J. Hill, Jr.

ASST-EXMR: Sally P. Teng LEGAL-REP: Pennie & Edmonds

US PAT NO: 5,426,177 [IMAGE AVAILABLE] L1: 2 of 3

ABSTRACT:

The present invention relates to the ciliary neurotrophic factor (CNTF) receptor, and provides for CNTF receptor nucleic acid and amino acid sequences. It also relates to (i) assay systems for detecting CNTF activity; (ii) experimental model systems for studying the physiologic role of CNTF; (ii) diagnostic techniques for identifying CNTF-related neurologic conditions; (iv) therapeutic techniques for the treatment of CNTF-related neurologic and muscular conditions, and (v) methods for identifying molecules homologous to CNTF and CNTFR.

CLAIMS:

CLMS(1)

What is claimed is:

1. Isolated and purified CNTF receptor comprising the amino acid sequence as depicted in FIG. 2(SEQ ID no. 1)

US PAT NO:

5,171,837 [IMAGE AVAILABLE]

L1: 3 of 3

DATE ISSUED:

Dec. 15, 1992

TITLE:

Peptide capable of binding interleukin 6 and an adsorbent

comprising the peptide immobilized on a carrier

INVENTOR:

Masao Tanihara, Kurashiki, Japan Kiichiro Oka, Kurashiki, Japan

ASSIGNEE:

Kuraray Co., Ltd., Okayama, Japan (foreign corp.)

APPL-NO:

07/582,831 Oct. 5, 1990

DATE FILED: ART-UNIT:

184

PRIM-EXMR:

Robert A. Wax Stephen Walsh

ASST-EXMR: LEGAL-REP:

Wegner, Cantor, Mueller & Player

US PAT NO:

5,171,837 [IMAGE AVAILABLE]

L1: 3 of 3

ABSTRACT:

A peptide being capable of binding to interleukin 6, and an adsorbent for interleukin 6 comprising the peptide immobilized on a carrier.

CLAIMS:

CLMS(1)

What is claimed is:

1. A peptide being capable of binding to interleukin 6 represented by the general formula:

H-X-A-Y-Z

- wherein A is a peptide segment selected from the group consisting of
- a peptide segment of the formula: -Gly-Thr-Val-His-Leu-Leu-Val-Asp-Val-Pro-Pro-Glu-Pro-Gln-Leu-Ser-Cys-Phe-Arg-Lys-,
- a peptide segment of the formula: -Arg-Lys-Phe-Gln-Asn-Ser-Pro-Ala-Glu-Asp-Phe-Gln-Glu-Pro-Cys-Gln-Tyr-Ser-Gln-Glu-Ser-,
- a peptide segment of the formula: -Thr-Ser-Leu-Pro-Gly-Asp-Ser-Val-Thr-Leu-Thr-Cys-Pro-Gly-Val-Glu-Pro-Glu-Asp-,
- a peptide segment of the formula: -Gln-Ala-Leu-Thr-Thr-Asn-Lys-Asp-Asp-Asp-Asp-Asn-Ile-Leu-Phe-Arg-Asp-Ser-Ala-,
- a peptide segment of the formula: -Trp-Asn-Ser-Ser-Phe-Tyr-Arg-Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys,
- a peptide segment of the formula: -Ser-Thr-Pro-Ser-Leu-Thr-Thr-Lys-Ala-Val-Leu-Leu-Val-Arg-Lys-Phe-Gln-Asn-Ser-Pro-Ala-Glu-Asp-,
- a peptide segment of the formula: -Asn-Pro-Arg-Trp-Leu-Ser-Val-Thr-Trp-Gln-Asp-Pro-His-Ser-,
- a peptide segment of the formula: -His-Ser-Trp-Asn-Ser-Ser-Phe-Tyr-Arg-

Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys, a peptide segment of the formula: -Pro-His-Ser-Trp-Asn-Ser-Ser-Phe-Tyr-Arg-Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys-, a peptide segment of the formula: -Asp-Pro-His-Ser-Trp-Asn-Ser-Ser-Phe-Tyr-Arg-Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys-, a peptide segment of the formula: -Gln-Asp-Pro-His-Ser-Trp-Asn-Ser-Ser-Phe-Tyr-Arg-Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys-, and a peptide segment of the formula: -Trp-Gln-Asp-Pro-His-Ser-Trp-Asn-Ser-Ser-Phe-Tyr-Arg-Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser -Lys-; each of X and Y is a single bond or an amino acid residue selected from the group consisting of Asp, Glu, Lys, Ala and a divalent group of the formula: -NH(CH.sub.2).sub.n -CO- (wherein n is an integer of 1 to 17), or a peptide segment composed of 2 to 10 amino acid residues selected from the above group bound to each other through a peptide bond; and Z is a hydroxyl group or an amino group.

CLMS(2)

2. A peptide according to claim 1, wherein A is a peptide segment of the formula: -Gly-Thr-Val-His-Leu-Leu-Val-Asp-Val-Pro-Pro-Glu-Glu-Pro-Gln-Leu-Ser-Cys-Phe-Arg-Lys-.

CLMS(3)

3. A peptide according to claim 1, wherein A is a peptide segment of the formula: -Arg-Lys-Phe-Gln-Asn-Ser-Pro-Ala-Glu-Asp-Phe-Gln-Glu-Pro-Cys-Gln-Tyr-Ser-Gln-Glu-Ser-.

CLMS(4)

4. A peptide according to claim 1, wherein A is a peptide segment of the formula: -Thr-Ser-Leu-Pro-Gly-Asp-Ser-Val-Thr-Leu-Thr-Cys-Pro-Gly-Val-Glu-Pro-Glu-Asp-.

CLMS(5)

5. A peptide according to claim 1, wherein A is a peptide segment of the formula: -Gln-Ala-Leu-Thr-Thr-Asn-Lys-Asp-Asp-Asp-Asn-Ile-Leu-Phe-Arg-Asp-Ser-Ala-.

CLMS(6)

6. A peptide according to claim 1, wherein A is a peptide segment of the formula: -Trp-Asn-Ser-Ser-Phe-Tyr-Arg-Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys.

CLMS(7)

7. A peptide according to claim 1, wherein A is a peptide segment of the formula: -Ser-Thr-Pro-Ser-Leu-Thr-Thr-Lys-Ala-Val-Leu-Leu-Val-Arg-Lys-Phe-Gln-Asn-Ser-Pro-Ala-Glu-Asp-.

CLMS(8)

8. A peptide according to claim 1, wherein A is a peptide segment of the formula: -Asn-Pro-Arg-Trp-Leu-Ser-Val-Thr-Trp-Gln-Asp-Pro-His-Ser-.

CLMS(9)

9. A peptide according to claim 1, wherein A is a peptide segment of the formula: -His-Ser-Trp-Asn-Ser-Ser-Phe-Tyr-Arg-Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys.

CLMS (10)

10. A peptide according to claim 1, wherein A is a peptide segment of the formula: -Pro-His-Ser-Trp-Asn-Ser-Ser-Phe-Tyr-Arg-Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys-.

CLMS (11)

11. A peptide according to claim 1, wherein A is a peptide segment of the formula: -Asp-Pro-His-Ser-Trp-Asn-Ser-Ser-Phe-Tyr-Arg-Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys-.

CLMS (12)

12. A peptide according to claim 1, wherein A is a peptide segment of the formula: -Gln-Asp-Pro-His-Ser-Trp-Asn-Ser-Ser-Phe-Tyr-Arg-Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys-.

CLMS (13)

13. A peptide according to claim 1, wherein A is a peptide segment of the formula: -Trp-Gln-Asp-Pro-His-Ser-Trp-Asn-Ser-Ser-Phe-Tyr-Arg-Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys-.

CLMS (14)

14. An adsorbent comprising the peptide according to claim 1 immobilized on a carrier.

CLMS (15)

15. An adsorbent comprising the peptide according to claim 2 immobilized on a carrier.

CLMS (16)

16. An adsorbent comprising the peptide according to claim 3 immobilized on a carrier.

CLMS (17)

17. An adsorbent comprising the peptide according to claim 4 immobilized on a carrier.

CLMS (18)

18. An adsorbent comprising the peptide according to claim 5 immobilized on a carrier.

CLMS (19)

19. An adsorbent comprising the peptide according to claim 6 immobilized on a carrier.

CLMS (20)

20. An adsorbent comprising the peptide according to claim 7 immobilized on a carrier.

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CLMS (21)

21. An adsorbent comprising the peptide according to claim 8 immobilized on a carrier.

CLMS (22)

22. An adsorbent comprising the peptide according to claim 9 immobilized on a carrier.

CLMS (23)

23. An adsorbent comprising the peptide according to claim 10 immobilized on a carrier.

CLMS (24)

24. An adsorbent comprising the peptide according to claim 11 immobilized on a carrier.

CLMS (25)

25. An adsorbent comprising the peptide according to claim 12 immobilized on a carrier.

CLMS (26)

26. An adsorbent comprising the peptide according to claim 13 immobilized on a carrier.

=> ds

L1

'DS' IS NOT A RECOGNIZED COMMAND

=> d his

(FILE 'USPAT' ENTERED AT 10:35:38 ON 03 JUL 96)

3 S HUMAN INTERLEUKIN 6 RECEPTOR?

=> s interleukin 6 receptor?

2317 INTERLEUKIN

1835874 6

23249 RECEPTOR?

L2 12 INTERLEUKIN 6 RECEPTOR?

(INTERLEUKIN(W) 6 (W) RECEPTOR?)

=> s antibod?

L3 19922 ANTIBOD?

=> s 13 and 12

L4 12 L3 AND L2

=> d 1-12

- 1. 5,476,774, Dec. 19, 1995, Quantitation of nucleic acids using the polymerase chain reaction; Alice M. Wang, et al., 435/91.2, 6, 320.1; 536/24.33; 935/77, 78 [IMAGE AVAILABLE]
- 2. 5,470,730, Nov. 28, 1995, Method for producing T.sub.H -independent

- cytotoxic T lymphocytes; Phillip D. Greenberg, et al., 435/172.3; 424/93.21; 435/69.1, 69.52, 70.4, 252.3, 320.1 [IMAGE AVAILABLE]
- 3. 5,462,731, Oct. 31, 1995, Use of IL-6 for the treatment of chronic lymphocyte leukemia (CLL) and B-cell lymphomas; Dan Aderka, et al., 424/85.2, 85.1; 514/12, 21; 530/351 [IMAGE AVAILABLE]
- 4. 5,447,851, Sep. 5, 1995, DNA encoding a chimeric polypeptide comprising the extracellular domain of TNF receptor fused to IgG, vectors, and host cells; Bruce A. Beutler, et al., 435/69.7, 69.5, 240.2, 320.1; 530/300, 351; 536/23.4 [IMAGE AVAILABLE]
- 5. 5,426,177, Jun. 20, 1995, Ciliary neurotrophic factor receptor; Samuel Davis, et al., 530/395, 350, 839 [IMAGE AVAILABLE]
- 6. 5,326,559, Jul. 5, 1994, Treatment of accelerated atheosclerosis with interleukin-2 receptor targeted molecules; D. Douglas Miller, 424/85.2, 144.1, 183.1; 435/69.5, 69.52, 69.7, 70.21; 514/2, 8, 21, 824; 935/106, 107, 109 [IMAGE AVAILABLE]
- 7. 5,223,611, Jun. 29, 1993, DNA encoding for human GP130 protein; Tadamitsu Kishimoto, 530/351; 435/69.1, 320.1; 536/23.5 [IMAGE AVAILABLE]
- 8. 5,219,727, Jun. 15, 1993, Quantitation of nucleic acids using the polymerase chain reaction; Alice M. Wang, et al., 435/6, 91.2, 91.21; 536/24.33; 935/77, 78 [IMAGE AVAILABLE]
- 9. 5,216,128, Jun. 1, 1993, IFN-.beta.2/IL-6 receptor its preparation and pharmaceutical compositions containing it; Daniela Novick, et al., 530/350, 351, 413, 416, 834 [IMAGE AVAILABLE]
- 10. 5,188,828, Feb. 23, 1993, Interleukin-6 to stimulate erythropoietin production; Mark A. Goldberg, et al., 424/85.2; 514/8, 12; 530/351 [IMAGE AVAILABLE]
- 11. 5,171,837, Dec. 15, 1992, Peptide capable of binding interleukin 6 and an adsorbent comprising the peptide immobilized on a carrier; Masao Tanihara, et al., 530/324, 325, 326, 810 [IMAGE AVAILABLE]
- 12. 5,132,403, Jul. 21, 1992, Human gp130 protein; Tadamitsu Kishimoto, 530/351, 350, 388.22 [IMAGE AVAILABLE]

=>

THE 1ST DEP. INTERNAL MED., NATL. DEFENCE MED. COLL., 3-2 NAMIKI, TOKOROZAWA, SAITAMA 359, JAPAN

CLIN EXP IMMUNOL 88 (1). 1992 75-83. CODEN: CEXIA

Full Journal Title: Clinical and Experimental Immunology

Language: ENGLISH

Introducing avidin-biotin complex ELISA for anti-DNA antibody, the mechanism of in vitro production of anti-ssDNA antibody as well as of immunoglobulin mediated by an IL-6-IL-6R loop was studied in patients with systemic lupus erythematosus (SLE). Regardless of presence or absence of T cells, B cells from SLE patients could produce IgG anti-ssDNA antibody as well as total IgG without any stimulation. Low density B cells obtained by Percoll gradient density centrifugation responded to rIL-6 to produce IgG and IgG anti-ssDNA antibody. rIL-2 and rIL-4 had lesser effects on the differentiation of low density B cells. In fact, IL-6R was preferentially expressed on low density B cells from active SLE patients, as detected by anti-IL-6R MoAb, MT18, which did not inhibit IL-6 binding. SLE B cells, especially high density B cells, produced greater amounts of IL-6 in culture supernatants than did T cells, regardless of whether disease was active or inactive. Normal T cells and B cells did not produce significant amounts of IL-6. Thus, endogenous IL-6 produced by high density B cells bound to the IL-6R preferentially expressed on the low density B cells, and drove them into terminal differentiation, especially in active SLE patients. Further, addition of polyclonal anti-IL-6 or anti-IL-6R MoAb (PM1), which inhibited IL-6 binding, both inhibited IgG anti-ssDNA antibody as well as total IgG production by SLE B cells in a dose-dependent manner. These results suggest that interruption of the autocrine IL-6 loop would be of therapeutic value in SLE.

16/7/6

DIALOG(R) File 55:BIOSIS PREVIEWS(R) (c) 1996 BIOSIS. All rts. reserv.

9032401 BIOSIS Number: 93017401

ANTI-MURINE IL-6 RECEPTOR ANTIBODY INHIBITS IL-6 EFFECTS IN-VIVO SUZUKI H; YASUKAWA K; SAITO T; ANZAI M; GOITSUKA R; HASEGAWA A; OHSUGI Y; TAGA T; KISHIMOTO T

INSTITUTE MOLECULAR CELLULAR BIOLOGY, OSAKA UNIV. 1-3, YAMADAOKA, SUITA-SHI, OSAKA 565, JAPAN.

IMMUNOL LETT 30 (1). 1991. 17-22. CODEN: IMLED

Full Journal Title: Immunology Letters

Language: ENGLISH

Thrombopoiesis, as well as antibody production, is one of the major events in which interleukin-6 (IL-6) has been reported to be involved. Polyclonal antimurine IL-6 receptor antibody was prepared to examine the effect of the antibody on these events in IL-6-treated mice. Administration of the anti-mIL-6R antibody inhibited the IL-6-induced increase in the number of platelets. Enhancement of the serum level of DNP-specific antibody by intraperitoneal injection of IL-6 was inhibited completely with simultaneous administration of the anti-mIL-6R antibody. The level of DNP-specific antibody was decreased, even below the basal value, by the higher dose of anti-mIL-6R antibody, indicating its effect also on endogenous Il-6. This work provides evidence that anti-IL-6R antibody inhibits IL-6 function in vivo, and provides an animal model of the therapeutic use of anti-IL-6R antibody for IL-6-related disease.

Get

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    (c) 1996 BIOSIS
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          12 S14 AND S15
?t s16/7/1-12
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DIALOG(R) File 55:BIOSIS PREVIEWS(R)
(c) 1996 BIOSIS. All rts. reserv.
10029465
            BIOSIS Number: 95029465
 ROLE OF INTERLEUKIN 6 IN THE GROWTH OF MYELOMA-DERIVED CELL LINES
 BARUT B A; ZON L I; COCHRAN M K; PAUL S R; CHAUHAN D; MOHRBACHER A;
FINGEROTH J; ANDERSON K C
 DIV. TUMOR IMMUNOL., DANA-FARBER CANCER INST., 44 BINNEY ST., BOSTON,
MASS. 02115.
 LEUK RES 16 (10). 1992. 951-959. CODEN: LERED
 Full Journal Title: Leukemia Research
 Language: ENGLISH
  The role of interleukin 6 (IL-6) in the growth of five multiple
```

myeloma-derived cell lines was characterized. The U266 and RPMI 8226 cells lines demonstrated increased DNA synthesis when cultured with exogenous IL-6, expressed IL-6 cell surface receptors (IL-6Rs) and expressed mRNA for IL-6R. However, these cells did not secrete detectable IL-6 protein, and a neutralizing antibody to IL-6 did not inhibit their growth. Three other myeloma-derived cells lines ARH-77, IM-9 and HS-Sultan did not respond to secrete IL-6 or express cell surface IL-6Rs. The IL-6 exogenous IL-6, responsive cell lines bore late B-cell surface antigens (Ags), CD38 and whereas those lines which were non-IL-6 responsive strongly expressed B1 (CD20) and B4 (CD19) Ags, representing earlier stages in B-cells differentiation. Finally, the two IL-6 responsive cell lines did not express Epstein-Barr virus (EBV) proteins; in contrast, EBV encoded proteins typically expressed during latency could be detected in the three non-IL-6 responsive lines, confirming infection with virus. These studies clarify the heterogeneity observed in the myeloma cell line phenotype and biology and suggest that the U266 and RPMI 8226 cells lines, which express IL-6 cell surface receptors and are IL-6 responsive, may be useful for further study of IL-6 signal transduction in and related IL-6 mediated growth of myeloma in vivo. In contrast, those cell lines which are IL-6-independent provide a model for further study of EBV transformation and IL-6-dependent growth mechanisms in malignancy.

16/7/2 DIALOG(R)File 55:BIOSIS PREVIEWS(R) (c) 1996 BIOSIS. All rts. reserv.

9787030 BIOSIS Number: 44037030

CLINICAL APPLICATIONS OF IL6 INHIBITORS

KLEIN B; LU Z Y; BATAILLE R

LAB. D'ONCOGENESE IMMUNOHEMATOL., INST. DE BIOL., 9 QUAI MONCOUSU, 44035 NANTES, FR.

RES IMMUNOL 143 (7). 1992. 774-776. CODEN: RIMME

Full Journal Title: Research in Immunology

Language: ENGLISH

16/7/3
DIALOG(R) File 55:BIOSIS PREVIEWS(R)
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9593256 BIOSIS Number: 94098256

ANTI-HUMAN INTERLEUKIN-6 RECEPTOR ANTIBODY INHIBITS HUMAN MYELOMA GROWTH IN-VIVO

SUZUKI H; YASUKAWA K; SAITO T; GOITSUKA R; HASEGAWA A; OHSUGI Y; TAGA T; KISHIMOTO T

DEP. MED. III, OSAKA UNIV. MED. SCH., 1-1-50 FUKUSHIMA, FUKUSHIMA-KU, OSAKA 553, JPN.

EUR J IMMUNOL 22 (8). 1992. 1989-1993. CODEN: EJIMA

Full Journal Title: European Journal of Immunology

Language: ENGLISH

Myeloma is one of the interleukin (IL)-6-related diseases to which abnormal expression of IL-6 has been reported to be linked. We examined the in vivo inhibitory effect of anti-human IL-6 receptor (IL-6R) antibody on human myeloma cell growth in mice. SCID mice were subcutaneously inoculated with solid tumor of the myeloma cell line S6B45 in which human IL-6 was acting as an autocrine growth factor. Ten intraperitoneal administrations of 100 .mu.g of the anti-human IL-6R antibody PM1 at 48-h intervals

strongly inhibited the growth of S6B45 cells when the administration started 24 h after tumor inoculation. The tumor growth inhibition in vivo was also observed by administration of the anti-human IL-6 antibody MH166 using the same procedure as for PM1. The inhibitory effect of PM1 was not significant when the administration started 5 or more days after tumor inoculation. This work indicates that anti-human IL-6R antibody, as well as anti-human IL-6 antibody inhibits human myeloma growth in vivo, and provides an animal model for testing the therapeutic value of agents such as antibodies to human IL-6, IL-6R and gp130, an IL-6R-associated signal transducer, in the treatment of human myelomas.

16/7/4
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9547472 BIOSIS Number: 94052472

INCREASE IN INTERLEUKIN 6 IL-6 AND IL-6 RECEPTOR EXPRESSION IN A HUMAN MULTIPLE MYELOMA CELL LINE U-266 DURING LONG-TERM IN-VITRO CULTURE AND THE DEVELOPMENT OF A POSSIBLE AUTOCRINE IL-6 LOOP

JERNBERG-WIKLUND H; PETTERSSON M; CARLSSON M; NILSSON K

LAB. TUMOR BIOLOGY, DEP. PATHOLOGY, UNIV. HOSP., S-751 85 UPPSALA, SWEDEN.

LEUKEMIA (BASINGSTOKE) 6 (4). 1992. 310-318. CODEN: LEUKE Language: ENGLISH

A human multiple myeloma (MM) cell line, U-266, has developed the ability to grow independently of exogenous interleukin 6 (IL-6) during long-term cultivation in vitro. The early passage, feeder-cell dependent U-266 cell line (U-266-1970) was compared with the late passage U-266-1984 cell line with respect to response to IL-6, IL-1.beta. and tumour necrosis factor .alpha. and expression of IL-6 and IL-6 receptor (IL-6R) mRNA and protein. The results showed that; (a) only the U-266-1970 cell line was stimulated to growth by IL-6, (b) IL-6 and IL-6R mRNA were expressed in both cell lines, (c) the level of IL-6 mRNA was increased in the U-266-1984 cell line and only this line produced IL-6 and, (d) the level of IL-6R mRNA was highest in the U-266-1984 cell line and the number of IL-6R about ten times higher than in U-266-1970. The growth of the IL-6-producing U-266-1984 cell was inhibited by 30% by anti-IL-6R antibodies suggesting the possibility that an autocrine IL-6 loop might have developed during the long-term cultivation. In addition to many other phenotypic alterations of the U-266 cell line, having developed as a consequence of tumor progression in vitro, its growth factor requirement seems to have evolved from a dependence on IL-6 as a paracrine growth factor to a capacity for autonomous growth, dependent on autocrine IL-6 stimulation. Whether such a development also may take place in MM clones in vivo remains to be established.

16/7/5
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9500353 BIOSIS Number: 94005353

AUTOSTIMULATORY EFFECTS OF IL-6 ON EXCESSIVE B CELL DIFFERENTIATION IN PATIENTS WITH SYSTEMIC LUPUS ERYTHEMATOSUS ANALYSIS OF IL-6 PRODUCTION AND IL-6R EXPRESSION

KITANI A; HARA M; HIROSE T; HARIGAI M; SUZUKI K; KAWAKAMI M; KAWAGUCHI Y; HIDAKA T; KAWAGOE M; NAKAMURA H

16/7/7
DIALOG(R) File 55:BIOSIS PREVIEWS(R)
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8588351 BIOSIS Number: 92053351

PREPARATION OF SOLUBLE MURINE IL-6 RECEPTOR AND ANTI-MURINE II-6 RECEPTOR ANTIBODIES

SAITO T; YASUKAWA K; SUZUKI H; FUTATSUGI K; FUKUNAGA T; YOKOMIZO C; KOISHIHARA Y; FUKUI H; OHSUGI Y; ET AL

DIV. IMMUNOL., INST. MOL. CELL. BIOL., OSAKA UNIV., 1-3 YAMADA-OKA, SUITA-SHI, OSAKA 565, JPN.

J IMMUNOL 147 (1). 1991. 168-173. CODEN: JOIMA

Full Journal Title: Journal of Immunology

Language: ENGLISH

Starting with a previously isoalted cDNA clone encoding murine IL-6R, a stable transformed Chinese hamster ovary cell line constitutively expressing soluble murine IL-6R (smIL-6R) has been established. The smIL-6R was purified to homogeneity by sequential filtration and chromatography of culture medium. The smIL-6R augmented the sensitivity of M1 cells to IL-6 in their growth inhibition in a dose-response manner. Rat hybridomas producing mAb specific to murine IL-6R were also established. One of the clones, RS13, produced IgG2a isotype that was capable of inhibiting IL-6 activity. ELISA for the quantitation of smIL-6R was established, which could detect smIL-6R in a quantity as low as 1 ng/ml.

16/7/8
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8564429 BIOSIS Number: 92029429

IL-6 AND TUMOR NECROSIS FACTOR-ALPHA AUTOCRINE AND PARACRINE CYTOKINES INVOLVED IN B CELL FUNCTION

RIECKMANN P; D'ALESSANDRO F; NORDAN R P; FAUCI A S; KEHRL J H LAB. IMMUNOREGULATION, NATIONAL INST. ALLERGY INFECTIOUS DISEASES, NIH,

BUILDING 10, ROOM 11 B 13, BETHESDA, MD. 20892.

J IMMUNOL 146 (10). 1991. 3462-3468. CODEN: JOIMA

Full Journal Title: Journal of Immunology

Language: ENGLISH

IL-6 and TNF-.alpha. are synthesized and secreted by normal tonsillar B cells after stimulation with the polyclonal B cell activator Staphylococcus aureus Cowan strain 1 (SAC) and IL-2 as well as spontaneously by in vivo activated B cells from patients with hypergammaglobulinemia. Using specific neutralizing antibodies, both factors were shown to be involved in autocrine and/or paracrine regulation of B cell differentiation. IqG induced by SAC/IL-2 stimulation was reduced 73% with an anti-IL-6 antibody and 40% with an anti-TNF-.alpha. antibody. Similar effects of these antibodies were observed on the spontaneous in vitro IqG production by lymphoblastic B cells from six patients with hypergammaglobulinemia. with SAC/IL-2-activated B cells revealed that the studies Kinetic anti-TNF-.alpha. antibody must be present at the beginning of the culture to exert an effect on Ig production, whereas the anti-IL-6 antibody reduced Ig production even if added as late as day 3. This sequential action of TNF-.alpha. and IL-6 on B cell differentiation was reflected by different kinetics of release of these two cytokines into the supernatant of SAC/IL-2 activated B cells; TNF-.alpha. peaked at 24 h and IL-6 at 96 h after stimulation. In addition, it was shown that IL-6 production by in vitro-activated B cells was partially blocked by an anti-TNF-.alpha.

antibody suggesting that TNF-.alpha. regulates IL-6 production in normal B cells via an autocrine pathway. We also investigated the effects of TGF-.beta. on TNF-.alpha. and IL-6 production by normal B cells. Although TGF-.beta. inhibited Ig production by in vitro-activated and in vivo-activated B cells, it did not inhibit the release of these cytokines from normal B cells. Furthermore, TGF-.beta. did not inhibit the induction of nuclear factor-IL-6 nor the expression of IL-6R on activated B cells. Thus, although the biologic effects of anti-IL-6 and TGF-.beta. on B cell Ig production are similar, their mechanisms of actions appear to be distinct.

16/7/9
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8209434 BIOSIS Number: 91130434

CYTOKINE REGULATION OF LOCALIZED INFLAMMATION INDUCTION OF ACTIVATED B CELLS AND IL-6-MEDIATED POLYCLONAL IGG AND IGA SYNTHESIS IN INFLAMED HUMAN GINGIVA

KONO Y; BEAGLEY K W; FUJIHASHI K; MCGHEE J R; TAGA T; HIRANO T; KISHIMOTO T; KIYONO H

DEP. ORAL BIOLOGY, UNIVERSITY ALABAMA BIRMINGHAM, UAB STATION, BIRMINGHAM, ALA. 35294.

J IMMUNOL 146 (6). 1991. 1812-1821. CODEN: JOIMA

Full Journal Title: Journal of Immunology

Language: ENGLISH

It is well established that increased numbers of plasma cells occur in localized tissues of chronic inflammatory diseases such as adult peridontitis, and enzymatic isolation has shown that most B lineage cells proudce IgG-subclass with some IgA-subclass responses. It would be of importance to determine if excess production of cytokines in the localized lesion account for these responses and in the present study we have assessed gingival mononuclear cell (GMC) supernatants for cytokines that activate B cells including IL-6R expression and for levels of IL-6 present. Inasmuch as limited numbers (.apprx.1 to 3 .times. 106 cells) of GMC were obtained from surgically removed tissues (.apprx. 400 mg), we have focused on the analysis of IL-6 production by GMC in this study. Further, initial evidence of additional cytokines that are produced by GMC and induce expression of IL-6R on resting B cells has been obtained. The GMC and PBMC from individual patients were cultured in the presence (or absence) of Con Higher levels of IL-6 were produced spontaneously by GMC when compared with Con A-stimulated PBMC. When PBMC cultures were supplemented with GMC supernatants obtained from the same patient, high numbers of spot-forming cells (SFC), mainly in IgG followed by IgA isotype, were seen. The induction of SFC by GMC supernatants was inhibited by incubation with a goat anti-human $\rm IL\textsupernatants$ on the effect of GMC supernatants on subclasses of PBMC SFC was determined, the response was IgG1 > IgG2 > IgG3 = IgG4 and IgA1 > IgA2, a pattern remarkably similar to the distribution of plasma cells in the GMC itself. To assess for cytokines in GMC supernatants that mediated B cell activation, supernatants containing anti-IL-6 were cultured with PBMC or purified B cells for 72 h. This treatment induced small proliferative B cell responses and elevated expression of IL-6R on B cells, but did not induce SFC responses. Further, incubation of B cells with GMC supernatants induced resting B cells (G0/G1) to enter the cell cycle (S and G2/M). Addition of human rIL-6 to these cultures on day 3 restored IgG- and IgA-subclass SFC responses by day 7. Cytokine-induced IL-6R expression also occured in vivo because freshly isolated GMC

expressed high levels of this receptor. These results show that GMC produce cytokines that induce B cell activation including IL-6R expression and secrete IL-6 that regulates B cell terminal differentiation into plasma cells of IgG- and IgA-subclasses. We are currently assessing the cytokines produced by GMC that induce the expression of IL-6R on B cells.

16/7/10
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8119517 BIOSIS Number: 91040517

INTERLEUKIN-6 IL-6 IS AN INTERMEDIATE IN IL-1-INDUCED PROLIFERATION OF LEUKEMIC HUMAN MEGAKARYOBLASTS

BRACH M A; LOWENBERG B; MANTOVANI L; SCHWULERA U; MERTELSMANN R; HERRMANN

DEP. HEMATOLOGY ONCOLOGY, UNIVERSITY FREIBURG MEDICAL CENTER, HUGSTETTERSTRASSE 55, D-7800 FREIBURG, GER.

BLOOD 76 (10). 1990. 1972-1979. CODEN: BLOOA

Full Journal Title: Blood

Language: ENGLISH

We have examined the in vitro effects of recombinant human (rh) interleukin-1 (IL-1) on the growth of purified megakaryoblasts obtained from patients with acute megakaryoblastic leukemia. We demonstrate that IL-1 alpha and IL-1 beta treatment of these cells led to stimulation of DNA synthesis (as shown by increase of 3H-thymidine incorporation up to 35-fold) and also resulted in colony formation of leukemic megakaryoblasts. However, the stimulatory effect of IL-1 was dependent on endogenous production of IL-6, because addition of neutralizing monoclonal antibody (MoAb) to IL-6 abrogated the stimulatory activity of IL-1. In contrast, neutralizing MoAbs to granylocyte (G)-colony stimulating factor (CSF), (GM)-CSF, and macrophage (M)-CSF failed tr granulocyte-macrophage counteract the growth-enhancing effects of IL-1. Leukemic megakaryoblasts accumulated IL-6 mRNA and released IL-6 protein into their culture supernatant when exposed to rh IL-1 but failed to disclose transcripts for G-, GM-, and M-CSF under these conditions. Analysis of IL-6 receptor (IL-6R) transcript levels demonstrated that megakaryoblasts constitutively expressed IL-6R mRNA and that these transcripts are down-regulated to undetectable levels upon exposure to IL-1 and IL-6. Increase of 3H-thymidine incorporation by megakaryoblasts could be duplicated by exogenous IL-6 that could be blocked by neutralizing MoAb to IL-6. In conclusion, our results suggest that leukemic megakaryogblasts could produce and secrete IL-6, and express IL-6R, and that the growth-enhancing effect of IL-1 on these cells is indirect, via production of IL-6 by leukemic cells.

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7743486 BIOSIS Number: 90111486

ASSOCIATION BETWEEN IL-6 AND CD40 SIGNALING IL-6 INDUCES PHOSPHORYLATION OF CD-40 RECEPTORS

CLARK E A; SHU G

REG. PRIMATE RES. CENT. SJ-50, CENT HEALTH SCI., UNIV. WASHINGTON, SEATTLE, WA 98195.

J IMMUNOL 145 (5). 1990. 1400-1406. CODEN: JOIMA

Full Journal Title: Journal of Immunology

Language: ENGLISH

CD40 mAb at subsaturating doses inhibit the growth of transformants of the M12 murine cell line expressing intact full length CD40 molecules (M12/CD40+ cells) but do not inhibit the growth of two M12 transformants expressing either a mutant CD40 cDNA missing most of the cytoplasmic tail (CD40/tailless) or a mutant cDNA with a substitution at residue 234 (CD40/23A, Ala for Thr). Using these transformants, we tested a panel of cytokines for the ability to mimic CD40 mAb. rIL-6 behaved like CD40 mAb and inhibited the growth of M12/CD40+ cells but not of CD40/tailless or CD40/234A mutants. The effect of IL-6 on M12/CD40+ cells not only required intact CD40 including threonine 234 but also was specific because IL-6 mAb blocked the inhibitory activity. The M12/CD40+ cells responsive to IL-6 expressed > 300,000 CD40 molecules/cells but, like M12/CD40-controls, expressed only small numbers (<50/cell) of high affinity IL-6R, indicating that CD40 is not a receptor for IL-6. Nevertheless, IL-6 utilizes intact CD40 efficiently when it signals these cells: treatment of M12/CD40+ cells with IL-6 induced increased phosphorylation of CD40. Conversely, triggering CD40 on M12/CD40+ cells leads to IL-6 production. Similar effects were evident in human CD40+ B cells: IL-6 increased the phosphorylation of CD40 in the IL-6-responsive cell line, CESS, and CD40 mAb induced IL-6 production in activated human B cells. Thus, CD40 may function to receive and regulate IL-6-dependent signals in B cells.

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7364057 BIOSIS Number: 89015076

CHARACTERIZATION OF IL-6 RECEPTOR EXPRESSION BY MONOCLONAL AND POLYCLONAL ANTIBODIES

HIRATA Y; TAGA T; HIBI M; NAKANO N; HIRANO T; KISHIMOTO T

DIV. IMMUNOL., INST. MOL. CELL. BIOL., OSAKA UNIV., 1-3 YAMADA-OKA, SUITA, OSAKA 565, JPN.

J IMMUNOL 143 (9). 1989. 2900-2906. CODEN: JOIMA

Full Journal Title: Journal of Immunology

Language: ENGLISH

mAb and polyclonal antibodies against human IL-6R were prepared by using a murine transfectant cell line expressing the human IL-6R and a synthetic oligopeptide made on the basis of the deduced amino acid sequence as immunogens. Immunoprecipitation of radiolabeled IL-6R with these antibodies showed that the Mr of a mature IL-6R was 80 kDa and its value was reduced 50K after treatment with O- and N-glycanase and neuraminidase, indicating that IL-6R is a glycoprotein. Two mAb recognizing different epitopes were prepared. One, PM1 inhibited the binding of 125I-IL-6 to the receptor and blocked the IL-6-dependent growth of a T lymphoma line, KT3. could not bind to IL-6R when it was saturated with IL-6, indicating that this antibody recognizes the IL-6 binding or the adjacent site on IL-6R. The other, MT18 was not inhibited by IL-6R, therefore, this could be used for cytofluorometric staining of normal cells. Nonstimulated B cells expressed undetectable amount of IL-6R regardless of the expression of surface IgD. However, after the stimulation with PWM, IL-6R was observed on IgD- B cells with a relatively large size, but subtly on IgD- small B cells and not on IgD+ B cells, fitting the function of IL-6 which acts on activated B cells to induce Ig production. In contrast, IL-6R was detected on non-stimulated CD4+/CD8- and CD4-/CD8+ T cells. The level of IL-6R on both T cell subpopulations was not significantly changed after stimulation

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                S4 AND S2
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                NEUTRALI? OR INHIBIT?
S15
                S14 AND S15
S16
           12
S17
           30
                HUMAN (W) IL (W) 6 (W) RECEPTOR?
?s s6 and s17
          259799 S6
              30
                  S17
     S18
              13
                  S6 AND S17
?s chimeric or humaniz? or reshap?
            8485 CHIMERIC
             442 HUMANIZ?
             185 RESHAP?
     S19
            9024 CHIMERIC OR HUMANIZ? OR RESHAP?
?s s18 and s19
              13
                  S18
            9024 S19
               1 S18 AND S19
     S20
2t s20/7/1
 20/7/1
DIALOG(R) File 55:BIOSIS PREVIEWS(R)
(c) 1996 BIOSIS. All rts. reserv.
             BIOSIS Number: 97239162
  Humanization of a mouse anti-human interleukin-6 receptor antibody
comparing two methods for selecting human framework regions
  Sato K; Tsuchiya M; Saldanha J; Koishihara Y; Ohsugi Y; Kishimoto T;
Bendiq M M
```

Chugai Pharm. Co. Ltd., Fuji-Gotemba Res. Labs, 1-135 Komakado,

Gotemba-shi, Shizuoka 412, JAP

Molecular Immunology 31 (5). 1994. 371-38 Full Journal Title: Molecular Immunology

ISSN: 0161-5890 Language: ENGLISH

Print Number: Biological Abstracts Vol. 097 Iss. 011 Ref. 156275

Mouse monoclonal antibody AUK12-20 binds to human IL-6 receptor and inhibits IL-6 functions. It has been humanized by CDR-grafting for therapeutic use. In the design of reshaped human AUK12-20 V-L region, the human framework regions (FRs) from the human Bence-Jones protein REI were used. The reshaped human AUK12-20 light chain, in combination with chimeric AUK12-20 heavy chain, bound to antigen as well as chimeric AUK12-20 In the design of reshaped human AUK12-20 V-H region, two sets of antibody. the human FRs were chosen and compared. One set was from the consensus acid sequence for human V-H regions subgroup (HSG)-I and the other set was from human antibody HAX, the most similar human V-H region found in a database of human immunoglobulin sequences. The HSG-I-based and the HAX-based reshaped human AUK12-20 heavy chains in combination with the reshaped human AUK12-20 light chain, showed approximately 90 and 100% antigen-binding and competition-binding activities as compared to the chimeric or mouse AUK12-20 heavy chains. Most importantly, these humanized inhibited the IL-6-dependent tumor cell growth as well as the antibodies original mouse antibody suggesting that these humanized antibodies could be efficacious in human patients. Our results show that both approaches for the design of reshaped human antibodies can be used for successful The approach based on FRs from the most similar individual humanization. human antibody, however, seemed to be best for designing a reshaped human antibody that mimicked as closely as possible the original mouse antibody. ?ds

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Set
        Items
                 Description
S1
          622
                 IL6
S2
       301812
                 RECEPTOR?
S3
        12338
                 INTERLEUKIN (W) 6
S4
        12505
                 S1 OR S3
S5
         2087
                 S4 AND S2
S6
       259799
                 ANTIBOD?
S7
          463
                 S5 AND S6
S8
          173
                 IL(W)6R
S9
           64
                 S6 AND S8
S10
          281
                 INTERLEUKIN (W) 6 (W) RECEPTOR?
S11
           63
                 S6 AND S10
S12
           99
                 S9 OR S11
S13
      1717319
                 PY=(1993:1996)
S14
           25
                 S12 NOT S13
S15
       483053
                 NEUTRALI? OR INHIBIT?
S16
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                 S14 AND S15
S17
           30
                 HUMAN (W) IL (W) 6 (W) RECEPTOR?
S18
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                 S6 AND S17
S19
         9024
                 CHIMERIC OR HUMANIZ? OR RESHAP?
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281 S10 259799 S6 9024 S19 S21 S10 AND S6 AND S19 21/7/1 DIALOG(R)File 55:BIOSIS PREVIEWS(R) (c) 1996 BIOSIS. All rts. reserv.

11039162 BIOSIS Number: 97239162

Humanization of a mouse anti-human interleukin-6 receptor antibody

comparing two methods for selecting human framework regions

Sato K; Tsuchiya M; Saldanha J; Koishihara Y; Ohsugi Y; Kishimoto T; Bendig M M

Chugai Pharm. Co. Ltd., Fuji-Gotemba Res. Labs, 1-135 Komakado, Gotemba-shi, Shizuoka 412, JAP

Molecular Immunology 31 (5). 1994. 371-381.

Full Journal Title: Molecular Immunology

ISSN: 0161-5890 Language: ENGLISH

Print Number: Biological Abstracts Vol. 097 Iss. 011 Ref. 156275

Mouse monoclonal antibody AUK12-20 binds to human IL-6 receptor and inhibits IL-6 functions. It has been humanized by CDR-grafting for therapeutic use. In the design of reshaped human AUK12-20 V-L region, the human framework regions (FRs) from the human Bence-Jones protein REI were used. The reshaped human AUK12-20 light chain, in combination with chimeric AUK12-20 heavy chain, bound to antigen as well as chimeric AUK12-20 antibody. In the design of reshaped human AUK12-20 V-H region, two sets of human FRs were chosen and compared. One set was from the consensus amino acid sequence for human V-H regions subgroup (HSG)-I and the other set was from human antibody HAX, the most similar human V-H region found in database of human immunoglobulin sequences. The HSG-I-based and the HAX-based reshaped human AUK12-20 heavy chains in combination with the reshaped human AUK12-20 light chain, showed approximately 90 and 100% antigen-binding and competition-binding activities as compared to the chimeric or mouse AUK12-20 heavy chains. Most importantly, these humanized antibodies inhibited the IL-6-dependent tumor cell growth as well as the original mouse antibody suggesting that these humanized antibodies could be efficacious in human patients. Our results show that both approaches for the design of reshaped human antibodies can be used for successful humanization. The approach based on FRs from the most similar individual human antibody, however, seemed to be best for designing a reshaped human antibody that mimicked as closely as possible the original mouse antibody.

21/7/2 DIALOG(R)File 55:BIOSIS PREVIEWS(R) (c) 1996 BIOSIS. All rts. reserv.

10110788 BIOSIS Number: 95110788

RESHAPING A HUMAN ANTIBODY TO INHIBIT THE INTERLEUKIN 6-DEPENDENT TUMOR CELL GROWTH

SATO K; TSUCHIYA M; SALDANHA J; KOISHIHARA Y; OHSUGI Y; KISHIMOTO T; BENDIG M M

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CANCER RES 53 (4). 1993. 851-856. CODEN: CNREA

Full Journal Title: Cancer Research

Language: ENGLISH

The mouse PM-1 monoclonal antibody binds to the human interleukin 6

receptor, inhibits IL-6 functions, and shows strong antitumor cell activity against multiple myeloma cells. In order to be effective as a therapeutic agent administered to human patients in repeated doses, reshaped human PM-1 antibodies consisting of human REI-based light chain and NEW-based heavy chain variable regions were designed and constructed with the assistance of a structural model of the mouse PM-1 variable regions. The best reshaped human PM-1 antibody is equivalent to mouse or chimeric PM-1 antibody in terms of antigen binding and growth inhibition against multiple myeloma cells. Only a few minor changes in the human framework regions were required to recreate the mouse PM-1 antigen-binding site within a human antibody. The reshaped human PM-1 antibody, therefore, could be efficacious in human multiple myeloma patients.

21795 PM 1252383 1 S22 278 PM(W)1 ?s s6 and s22

259799 S6 278 S22 S23 24 S6 AND S22 ?t s23/7/1-23

23/7/1 DIALOG(R)File 55:BIOSIS PREVIEWS(R) (c) 1996 BIOSIS. All rts. reserv.

12222771 BIOSIS Number: 98822771

Purification and characterization of salivary kallikrein from an insectivore (Scalopus aquaticus): Substrate specificities, immunoreactivity and kinetic analyses

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Archives of Biochemistry and Biophysics 329 (1). 1996. 104-112.

Full Journal Title: Archives of Biochemistry and Biophysics

ISSN: 0003-9861 Language: ENGLISH

Print Number: Biological Abstracts Vol. 101 Iss. 012 Ref. 173193

report the successful one-step separation of tissue kallikrein from the salivary glands of an insectivore, the Eastern Atlantic mole (Scalopus aquaticus) by perfusion chromatography. Purified mole salivary kallikrein characterized as a 30-kDa serine proteinase with a pI of 5.3 and a pH It was readily recognized by human tissue kallikrein antibody in immunoblot analyses. It preferentially hydrolyzes fluorogenic peptidyl substrates with arginyl residues, rather than lysyl residues at P1 substrate recognition site, indicating that it is like other mammalian kallikreins. Mole kallikrein efficiently releases kinin from low molecular weight human, dog, and bovine kininogen substrates with specific similar to that of human tissue kallikrein. Steady state activities kinetics performed with the synthetic tripeptidyl substrates, Phe-Phe-Arq-, Pro-Phe-Arg-, and Val-Leu-Arg-7-amino-4-methylcoumarin, gave K-m values for kallikrein of 3.3, 46.1, and 2.8 mu-M, respectively, and specificity constants, k-cat/K-m, of 3818, 165, and 8714 s-1 pM-1, respectively. Mole kallikrein, when compared with human and rat tissue kallikreins, more closely resembles human kallikrein based on immunoreactivity and kininogenase activity. Mole kallikrein appears to be a member of a single gene or small multigene family. S. aquaticus is recommended for studying the evolution of mammalian proteins and may offer advantages over rodent models for biomedical research.

23/7/2 DIALOG(R)File 55:BIOSIS PREVIEWS(R) (c) 1996 BIOSIS. All rts. reserv.

12032670 BIOSIS Number: 98632670

Two consecutive nucleotide substitutions resulting in the T3 receptor beta gene resulting in an 11-amino acid truncation in a patient with generalized resistance to thyroid hormone

Miyoshi Y; Nakamura H; Sasaki S; Tagami T; Misaki T; Konishi J; Nakao K 2nd Div., Dep. Internal Med., Hamamatsu Univ. Sch. Med., 3600 Hamadacho, Hamamatsu 431-31, Japan

Molecular and Cellular Endocrinology 114 (1-2). 1995. 9-17.

Full Journal Title: Molecular and Cellular Endocrinology

ISSN: 0303-7207 Language: ENGLISH

Print Number: Biological Abstracts Vol. 101 Iss. 004 Ref. 048415

identified unusual mutations in the T3 receptor (TR) beta gene in a 6-year-old Japanese girl with generalized resistance to thyroid hormone. Two consecutive base substitutions, T to A and C to A at nucleotide positions 1637 and 1638, respectively, changed the 451st codon coding for an 11-amino acid (TAA), resulting in stop codon to carboxyl(C)-terminus truncation. The patient was a heterozygote. Western blotting using an anti-TR antibody demonstrated the truncated receptor protein. The patient showed severe mental retardation (IQ41), disturbance speech development, and attention deficit hyperactivity disorder. Thyroid functional status by clinical evaluation was considered within the normal range in spite of high serum thyroid hormone levels (T4 725.9 nmol/1, T3 12.7 nmol/1, FT4 166.0 pmol/1). TSH increased from 0.6 to 24 mU/L after TRH (150 mu-g) injection. TSH secretion as well as 123I-uptake was suppressed only partially by T3 (75 mu-g/day for a week). Close examination of thyroid functions and TR-beta gene analysis were not possible in the family, except for paternal grandmother and one of her two sisters who showed no abnormality. The patient's truncated TR-beta showed very low T3 binding activity (K-a = 0.1 times 10-10 M), transcriptional activity, and a very strong dominant negative effect. When co-expressed with wild-type TR-beta at the molar ratio 1:1 in CV-1 cells, the mutant receptor inhibited the wild-type TR-beta transcriptional activity by 74% at 10 nM T3. Even 1 mu-M T3 could not normalize these impaired functions.

23/7/3
DIALOG(R) File 55:BIOSIS PREVIEWS(R)
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11772862 BIOSIS Number: 98372862

The regulatory site of functional GTP binding protein coupled to the high affinity cholecystokinin receptor and phospholipase A-2 pathway is on the G-beta subunit of G-q protein in pancreatic acini

Tsunoda Y; Owyang C

Dep. Internal Med., Univ. Mich., Ann Arbor, MI 48109, USA Biochemical and Biophysical Research Communications 211 (2). 1995. 648-655. Full Journal Title: Biochemical and Biophysical Research Communications

ISSN: 0006-291X Language: ENGLISH

Print Number: Biological Abstracts Vol. 100 Iss. 005 Ref. 064700

A non-hydrolysable guanosine nucleotide analog, GTP(S) at 200 mu-M, stimulated amylase secretion which was inhibited by an anti-phospholipase A-2 (PLA-2) antibody in permeabilized pancreatic acini, indicating that the PLA-2 pathway is linked to the GTP binding protein. A high affinity cholecystokinin (CCK) receptor agonist, CCK-OPE (10 mu-M), and a low affinity receptor agonist, $\overline{\text{CCK-8}}$ ($\overline{\text{O}}.1$ mu-M), both caused amylase secretion in permeabilized cells. The action of CCK-OPE was abolished by the GB antibody but not by the G-alpha-q,11 antibody, whereas the opposite was true of the CCK-8 response. Biscoclaurine alkaloid isotetrandrine (10 mu-M), a specific inhibitor of PLA-2-coupled G proteins, abolished Ca-2+ oscillations and amylase secretion induced by CCK-OPE (0.1100 nM), but not CCK-8 (10 pM) in intact acini. Gp antagonist-2A (10 mu-M), which inhibits the activation of Gq, also inhibited the actions of CCK-OPE (10 pM-1 mu-M) in intact acini. These observations indicate that the functional unit of the heterotrimeric G protein coupled to the high affinity CCK receptor appears to be different from that linked to the low affinity CCK receptor/G-q-alpha pathway. The regulatory site of this G protein coupled to the high affinity CCK receptor is on the beta subunit of G-q protein which elicits Ca-2+ oscillations and monophasic amylase secretion via the PLA-2 pathway.

23/7/4
DIALOG(R)File 55:BIOSIS PREVIEWS(R)
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11490979 BIOSIS Number: 98090979

Subclinical hypothyroidism resulting from autoimmune thyroiditis in female patients with endogenous depression

Custro N; Scafidi V; Lo Baido R; Nastri L; Abbate G; Cuffaro M P; Gallo S; Vienna G; Notarbartolo A

Cattedra di Patologia Medica, Via del Vespro 141, 90127 Palermo, Italy Journal of Endocrinological Investigation 17 (8). 1994. 641-646.

Full Journal Title: Journal of Endocrinological Investigation

ISSN: 0391-4097 Language: ENGLISH

Print Number: Biological Abstracts Vol. 099 Iss. 005 Ref. 061389

Thyroid function and presence of thyroid autoantibodies were assessed in a group of 75 consecutive female patients with mood disturbances and in a group of 38 healthy women of similar age recruited as controls. Nine patients suffered from major (endogenous) depression and 66 from minor (neurotic) depression. The individual patients had normal values of circulating thyroid hormones. Nevertheless, endogenously depressed patients had total serum triiodothyronine (M +- SE=1.49+-0.09 nmol/1) and both total (83.9+-4.3 nmol/1) and free serum thyroxine (13.9 +- 1.1 pmol/1) lower than in the group of minor depressed and in the group of controls (p lt 0.01, in both comparison). The median value of serum thyrotropin was 5.22 mU/l in the major depressed patients versus 1.72 mU/l in the minor depressed and 1.69 mU/l in the controls. Thyroid function test results in the minor depressed group did not significantly differ from those in the controls. Five of the 9 endogenously depressed patients were subclinically hypothyroid, while none of the 66 patients with minor depressive disorder showed thyroid dysfunction. Antibodies against thyroglobulin and/or thyroid peroxidase were positive in all the 5 endogenously depressed women with subclinical hypothyroidism, revealing a symptomless autoimmune thyroiditis, which was also confirmed by ultrasonography in all cases and histopathologically demonstrated in one case. None of the endogenously depressed women without thyroid dysfunction and none of the 66 minor depressives were seropositive for thyroid autoantibodies. Only one of the non-depressed women in the control group was found seropositive for TPO-Ab and showed an exaggerated TSH responsiveness to TRH stimulation. The findings indicate the possibility that endogenous depression is accompanied by latent hypothyroidism in an appreciable proportion of women. The detection of thyroid autoantibodies in such patients suggests that affective disorders might play a precipitating role in the development of thyroid autoimmune disease. Therefore, the possibility of immunological damage should be taken into consideration whenever depressed women display biochemical thyroid dysfunction.

23/7/5
DIALOG(R)File 55:BIOSIS PREVIEWS(R)
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11413460 BIOSIS Number: 98013460

Transforming growth factor beta 2 is the predominant isoform in the neural retina, retinal pigment epithelium-choroid vitreous of the monkey eye

Pfeffer B A; Flanders K C; Guerin C J; Danilepour D; Anderson D H Storz Div. American Cyanamid, Build. 96, Room 225A, 401 N. Middletown Road, Pearl River, NY 10965, USA

Experimental Eye Research 59 (3). 1994. 323-333.

Full Journal Title: Experimental Eye Research

ISSN: 0014-4835 Language: ENGLISH

Print Number: Biological Abstracts Vol. 099 Iss. 001 Ref. 013460

Several techniques were utilized to assess the levels, disposition and cellular sources of isoforms 1 and 2 of transforming growth factor beta (TGF-beta) in the posterior pole of the monkey eye. Freshly dissected tissues, as well as the saline vehicles in which dissections were performed, were analysed by sandwich enzyme-linked immunosorbent assay. In all tissues TGF-beta-2 was the predominant isoform, with beta-2:beta-1 ratios of 6: 1 for neural retina (as ng g-1) and 425:1 for vitreous (as 1-1). Retinal pigment epithelium (RPE)-Bruch's membrane-choroid complex contained approximately 10 times the amount of both TGF-beta isoforms as neural retina. For first passage cultures of monkey RPE, TGF-beta-2, but not TGF-beta-1, accumulated over time in conditioned media samples. Immunoreactivity for TGF-beta-2 was detected both in tissue sections of posterior pole, specifically in rod outer segments and RPE, and also in the first passage cultures of RPE. Antibodies to specific peptide sequences of both isoforms localized TGF-beta to the outer segments of rod photoreceptors. The apparent sequestration of TGF-beta-2 in photoreceptor outer segments, as well as the in vitro evidence for possible synthesis and release by RPE, suggest that TGF-beta-2 is an important modulator of visual function acting at the retina-RPE interface.

23/7/6
DIALOG(R)File 55:BIOSIS PREVIEWS(R)
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11249497 BIOSIS Number: 97449497

Cryptic nature of envelope V3 region epitopes protects primary monocytotropic human immunodeficiency virus type 1 from antibody neutralization

Bou-Habib D C; Roderiquez G; Oravecz T; Berman P W; Lusso P; Norcross M A Div. Hematol. Products, Center Biol. Evaluation Res., Food Drug Administration, NIH, Building 29A, Room 3B10, 8800 Rockville Pike, HFM-541, Bethesda, MD 20892, USA

Journal of Virology 68 (9). 1994. 6006-6013.

Full Journal Title: Journal of Virology

ISSN: 0022-538X Language: ENGLISH

Print Number: Biological Abstracts Vol. 098 Iss. 008 Ref. 103809

Characterization of biological and immunological properties of human immunodeficiency virus type 1 (HIV-1) is critical to developing effective therapies and vaccines for AIDS. With the use of a novel CD4+ T-cell line both monocytotropic (MT) permissive to infection by T-cell-tropic virus types, we present a comparative analysis of the immunological properties of a prototypic primary $\overline{\text{MT}}$ isolate of $\overline{\text{HIV-1}}$ strain with those of a T-cell-tropic variant (T-CSF) of the same (MT-CSF) which emerged spontaneously in vitro. The parental MT-CSF infected virus, only PM-1 cells and was markedly resistant to neutralization by sera from HIV-1-infected individuals, rabbit antiserum to recombinant MT-CSF gp120, and anti-V3 monoclonal antibodies. The T-CSF variant infected a variety of CD4+ T-cell lines, contained positively charged amino acid substitutions in gp120 V3 region, and was highly sensitive to antibody neutralization. Neutralization and antibody staining of T-CSF-expressing cells were significantly inhibited by HIV-1 V3 peptides; in contrast, the MT strain weak V3-specific binding of polyclonal and monoclonal only antibodies. Exposure of PM-1 cells to a mixture of both viruses in the presence of human anti-HIV-1 neutralizing antiserum resulted in infection with only MT-CSF. These results demonstrate that although the V3 region of viruses is immunogenic, the target epitopes in the V3 principal neutralizing domain on the membrane form of the MT envelope appear to be cryptic or hidden from blocking antibodies.

23/7/7
DIALOG(R) File 55:BIOSIS PREVIEWS(R)
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10930136 BIOSIS Number: 97130136

Direct and correlated responses to multitrait, divergent selection for immunocompetence

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Poultry Science 73 (1). 1994. 18-32.

Full Journal Title: Poultry Science

ISSN: 0032-5791 Language: ENGLISH

Print Number: Biological Abstracts Vol. 097 Iss. 006 Ref. 079999

Leghorn lines had been selected for an immunocompetence index based on four traits: antibody production to Mycoplasma gallisepticum (MG) and Pasteurella multocida (PM) vaccines, reticuloendothelial clearance of colloidal carbon (CCA), and cell-mediated, wing web response to phytohemagglutinin (PHA). The purpose of this study was to produce replicated lines of chickens with divergent levels of multitrait immunocompetence by index selection. The objectives of analyses of Generations 5 to 7 of this study was to characterize these lines with

respect to immune-response traits, correlations among these traits, and correlated responses in other important production traits. Differences (P lt .05) existed between the lines selected for high or low immune response and between the two replicates in mean breeding values and in individual immune-response traits. Averages of heritability estimates, weighted by number of offspring and pooled across three generations (two cycles of by using sire variance components selection), estimated parent-offspring correlations were, respectively, .16 and .09 for the index, .31 and .08 for MG, .21 and -.02 for PM, .06 and .05 for CCA, and .08 and .12 for PHA. Realized heritabilities (response divided by effective selection differential) pooled across the two selection cycles, were .19 and .11 for the index, .06 and -.01 for MG, .44 and .32 for PM, 1.52 and -1.21 for CCA, and .48 and. 15 for PHA, for Replicates 1 and 2, respectively. Phenotypic correlations among traits were generally small, and several estimates were negative. Estimates of genetic correlation varied widely. Juvenile and adult body weights, age of first egg, 32-wk egg weight, and rate of egg production were analyzed to evaluate effects of selection on these traits of direct economic importance. Very few differences were noted.

23/7/8
DIALOG(R)File 55:BIOSIS PREVIEWS(R)
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10110788 BIOSIS Number: 95110788

RESHAPING A HUMAN ANTIBODY TO INHIBIT THE INTERLEUKIN 6-DEPENDENT TUMOR CELL GROWTH

SATO K; TSUCHIYA M; SALDANHA J; KOISHIHARA Y; OHSUGI Y; KISHIMOTO T; BENDIG M M

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CANCER RES 53 (4). 1993. 851-856. CODEN: CNREA

Full Journal Title: Cancer Research

Language: ENGLISH

The mouse PM-1 monoclonal antibody binds to the human interleukin 6 receptor, inhibits IL-6 functions, and shows strong antitumor cell activity against multiple myeloma cells. In order to be effective as a therapeutic agent administered to human patients in repeated doses, reshaped human PM-1 antibodies consisting of human REI-based light chain and NEW-based heavy chain variable regions were designed and constructed with the assistance of a structural model of the mouse PM-1 variable regions. The best reshaped human PM-1 antibody is equivalent to mouse or chimeric PM-1 antibody in terms of antigen binding and growth inhibition against multiple myeloma cells. Only a few minor changes in the human framework regions were required to recreate the mouse PM-1 antigen-binding site within a human antibody. The reshaped human PM-1 antibody, therefore, could be efficacious in human multiple myeloma patients.

23/7/9
DIALOG(R) File 55:BIOSIS PREVIEWS(R)
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10098735 BIOSIS Number: 95098735
DEVELOPMENT OF MONOCLONAL ANTIBODIES SPECIFIC FOR 1 N-2
ETHENODEOXYGUANOSINE AND N-2 3 ETHENODEOXYGUANOSINE AND THEIR USE FOR QUANTITATION OF ADDUCTS IN G12 CELLS EXPOSED TO CHLOROACETALDEHYDE

FOILES P G; MIGLIETTA L M; NISHIKAWA A; KUSMIEREK J T; SINGER B; CHUNG

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CARCINOGENESIS (OXF) 14 (1). 1993. 113-116. CODEN: CRNGD

Language: ENGLISH

N2,3-ethenodeoxyguanosine antibodies specific for Monoclonal (N2,3-.epsilon.dGuo) and 1,N2-ethenodeoxyguanosine (1,N2-.epsilon.dGuo) were developed. In a competitive ELISA, 50% inhibition of binding of the N2,3-.epsilon.dGuo specific antibody (ETH1) was achieved with 18 fmol of inhibition of the N2,3-.epsilon.dGuo. Fifty per cent required 11 pmol (ETH2) 1,N2-.epsilon.dGuo-specific antibody N2,3-.epsilon.dGuo for Immunoassays 1.N2-.epsilon.dGuo. 1,N2-.epsilon.dGuo in single-stranded DNA were developed using these antibodies. The immunassays could detect as little as 48 fmol N2,3-.epsilon.dGuo or 340 fmol 1,N2-.epsilon.dGuo in 25 .mu.g of single stranded DNA. These assays and previously developed immunoassays for 1,N6-ethenodeoxyadenosine (1,N6-.epsilon.dAdo) and 3,N4-ethenodeoxycytidine (3,N4-.epsilon.dCyd) were used to measure etheno adduct levels in DNA of cells exposed to chloroacetaldehyde. The cells used were V79 cells with an inactivated hprt gene and a single copy of the bacterial gpt gene (G12 cells). The most abundant etheno adduct was 1,N6-.epsilon.dAdo, followed by 3,N4-.epsilon.dCyd and N2,3-.epsilon.dGuo. 1,N2-.epsilon.dGuo was not detected in chloroacetaldehyde-treated G12 cells. Chloroacetaldehyde was also shown to be mutagenic in these same cells.

23/7/10
DIALOG(R) File 55:BIOSIS PREVIEWS(R)
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10020207 BIOSIS Number: 95020207

INCREASED TISSUE CONCENTRATIONS OF THE GASTRIN PRECURSOR IN PATIENTS TREATED WITH OMEPRAZOLE

NEMETH J; VARRO A; BRIDSON J; WALKER R; DOCKRAY G J

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EUR J CLIN INVEST 22 (10). 1992. 638-644. CODEN: EJCIB

Full Journal Title: European Journal of Clinical Investigation

Language: ENGLISH

The main form of gastrin in antral mucosa, the amidated heptadecapeptide G17, is generated from an inactive precursor, progastrin, involving endopeptidase cleavage and amidation. Gastrin cells are normally inhibited by gastric acid and in this study we have examined how suppression of acid by treatment with omeprazole for 6-8 weeks influences gastrin production in patients with oesophagitis. Plasma concentrations of total amidated gastrins in the fasting state increased from 18 to 43 pmol assays specific for G17-immunoreactivity indicated that the plasma concentrations of this form increased from 6 to 12 pmol1-1. In endoscopic biopsies of antral mucosa there was no change with omepraxole treatment in of total amidated gastrins, or their immediate concentrations precursors, the Gly-extended gastrins. However, assays using an antibody that reacts with progastrin, together with size exclusion chromatography, indicated that tissue progastrin concentration increased 6-fold. The data modest net increase in gastrin production suggest a omeprazole-treatment; because the ratio of tissue concentrations of total amidated gastrins to Gly-extended gastrins did not change, it would seem that the amidating capacity of the gastrin cell was maintained. However,

the increase in progastrin concentrations suggests a relative failure of the initial steps of post-translational processing, and consequently that in certain circumstances endopeptidase cleavage of progastrin may be rate limiting.

23/7/11 DIALOG(R)File 55:BIOSIS PREVIEWS(R) (c) 1996 BIOSIS. All rts. reserv.

9143686 BIOSIS Number: 93128686

TROPHOBLAST-DERIVED TUMOR NECROSIS FACTOR-ALPHA INDUCES RELEASE OF HUMAN CHORIONIC GONADOTROPIN USING INTERLEUKIN-6 IL-6 AND IL-6-RECEPTOR-DEPENDENT SYSTEM IN THE NORMAL HUMAN TROPHOBLASTS

LI Y; MATSUZAKI N; MASUHIRO K; KAMEDA T; TANIGUCHI T; SAJI F; YONE K; TANIZAWA O

1-1-50 FUKUSHIMA, FUKUSHIMA-KU, OSAKA 553, JPN.

J CLIN ENDOCRINOL METAB 74 (1). 1992. 184-191. CODEN: JCEMA

Full Journal Title: Journal of Clinical Endocrinology & Metabolism

Language: ENGLISH

The titer of tumor necrosis factor-.alpha. (TNF.alpha.) secreted by placental blocks was determined by enzyme immunoassay. The source of placental TNF.alpha. was immunohistochemically demonstrated with monoclonal anti-TNF.alpha. antibody to be only trophoblasts. Purified trophoblasts produced 174.4 ng/L TNF.alpha. by 24 h of culture in vitro. To investigate the role of TNF.alpha. in placental hormonogenesis, purified trophoblasts were stimulated with recombinant TNF.alpha. (rTNF.alpha.) to determine the hCG titer by enzyme immunoassay. Trophoblasts stimulated with rTNF.alpha. released hCG in a dose-dependent fashion with kinetics similar to those of recombinant interleukin-1 (rIL-1)-stimulated trophoblasts. The stimulated trophoblasts released IL-6 before hCG, but failed to show hCG release when pretreated with anti-IL-6 receptor (anti-IL-6R) monoclonal antibody PM-1. However, the pretreatment of trophoblasts with PM-1 did not interfere with rTNF-.alpha.-induced IL-6 release, ruling out the possibility of nonspecific toxic effect of PM-1 on trophoblasts. These results suggest that trophoblast-derived TNF.alpha. induced IL-6 release and then activated the IL-6 -R system in trophoblasts to release hCG. Since IL-1 has also been demonstrated to induce similar release of IL-6 and hCG from trophoblasts, the effects of TNF.alpha. and IL-1 on these trophoblast functions were also Simultaneous stimulation of trophoblasts with rTNF.alpha. and .gamma.IL-1.alpha. resulted in synergistic enhancement of IL-6 release, enhanced hCG release. Collectivity, subsequently leading to trophoblast-derived TNF.alpha. and IL-1 synergistically regulated the level IL-6 secreted by trophoblasts, the magnitude of which determined the level of hCG released by activating the IL-6-R system in trophoblasts.

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9113449 BIOSIS Number: 93098449

RADIO-IMMUNOASSAY OF ENDOTHELIN IN HUMAN PLASMA

SORENSEN S S

DEP. NEPHROLOGY MED. C, SKEJBY HOSP., DK-8200 AARHUS C, DENMARK. SCAND J CLIN LAB INVEST 51 (7). 1991. 615-623. CODEN: SJCLA

Full Journal Title: Scandinavian Journal of Clinical and Laboratory Investigation

Language: ENGLISH

Endothelin (ET) is a newly described endothelium-derived 21-amino-acid peptide with potent vasoconstrictive properties. The present study describes a radio-immunoassay utilizing an antibody without cross-reactivity with big endothelin, produced after immunization of rabbits with endothelin-1 (ET-1). Measurement of endothelin in human plasma was performed after prior extraction on Sep-pak C18 cartridges. Recovery of unlabelled endothelin-1 added to human plasma (3.5 pg ml-1) was 84.8 .+-. 11.1% (mean .+-. SD, n = 12). The minimum detectable level in plasma was 50 fmol l-1. High-pressure liquid chromatography on reverse-phase C18 column established that the measured irET eluted identically to ET-1. The concentration of irET in plasma from healthy control subjects was 1.11 .+-. 0.2 pmol-1 (mean .+-. SD, n = 30). Agarose electrophoresis of plasma with [1251]-ET-1 indicated a reversible binding to albumin. It is concluded that ET-1 is present in measurable amounts in human plasma. It is suggested that ET-1 in plasma is associated with albumin. The importance of an adequate extraction procedure is stressed.

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9112746 BIOSIS Number: 93097746

DETERMINATION OF PLASMA CHOLECYSTOKININ CCK CONCENTRATIONS BY BIOASSAY AND RADIOIMMUNOASSAY IN MAN A CRITICAL EVALUATION

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REGUL PEPT 37 (3). 1992. 255-269. CODEN: REPPD

Full Journal Title: Regulatory Peptides

Language: ENGLISH

The present investigation was designed to perform a direct comparison of a rat pancreatic acini bioassay system and a specific CCK radioimmunoassay (antiserum G-160) for the measurement of fasting and meal-stimulated plasma CCK in the presence and absence of the CCK receptor antagonist loxiglumide. The G-160 CCK antiserum is directed against the C-terminal O-sulfated tyrosine residue of the CCK molecule which is essential for full bioactivity of CCK peptides. For plasma extraction prior to bioassay measurement, hydrophobic reverse-phase chromatography on octadecylsilane cartridges was employed and resulted in simultaneous adsorption and elution of both CCK peptides and loxiglumide with recoveries of 87.5 .+-. 9% and .+-. 5.9%, respectively. In the absence of loxiglumide, fasting and mealk-stimulated values for CCO-like bioactivity and CCK-immunoreactivity (IR-CCK) were nearly identical (basal values: 1-2 pmol/1; meal-stimulated plateau levels; 4-6 pmol/l). After intravenous infusion of loxiglumide (30 mg/kg/h for 10 min, 10 mg/kg/h thereafter), resulting in plasma steady state levels of 200-300 .mu.mol/l, meal-stimulated CCK-like bioactivity was undetectable, whereas IR-CCK levels were augmented 6.5-fold. bioassay system, standard samples containing 50 .mu.mol/l loxiglumide produced complete inhibition of acinar lipase release in response to 50 pmol/l synthetic CCK-8. We conclude, that postprandial circulating non-CCK-like factors do not contribute significantly to the direct receptor-mediated stimulation of exocrine pancreatic secretion. The good agreement of CCK-like bioactivity and IR-CCK levels in the absence of loxiglumide confirms the sensitive and specific recognition of bioactive

CCK peptides by the G-160 antiserum and suggests that this antibody exerts binding characteristics probably similar to a pancreatic acinar receptor.

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9020358 BIOSIS Number: 93005358

EARLY UNDIFFERENTIATED CONNECTIVE TISSUE DISEASE II. THE FREQUENCY OF CIRCULATING ANTINUCLEAR ANTIBODIES IN PATIENTS WITH EARLY RHEUMATIC DISEASES

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J RHEUMATOL 18 (9). 1991. 1340-1343. CODEN: JRHUA

Full Journal Title: Journal of Rheumatology

Language: ENGLISH

The presence of antinuclear antibodies (ANA) in the serum is a common finding in various connective tissue disorders, but usefulness of these antibodies in making diagnoses or prognoses is not known. We report the results of a panel of ANA determinations including ANA, anti-dsDNA, Sm, SSA, SSB, Jo-1, Scl-70 and PM-1 in 410 patients in a 5-year descriptive study of 410 patients with rheumatic disease symptoms of less than one year's duration. While some patients met diagnostic criteria for a classified rheumatologic diagnosis, others were specific undifferentiated connective tissue disease (UCTD) and were subclassified by a constellation of symptoms. Our results show that ANA is sensitive in systemic lupus erythematosus (SLE) and progressive systemic sclerosis even in early disease but is not specific. Other "specific" autoantibodies were seen most frequently in SLE but were relatively insensitive and were seen in low frequency in UCTD. ANA have limited diagnostic value in patients with early disease. The prognostic value of these tests will be assessed as the prospective study of these cohorts progresses.

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8085593 BIOSIS Number: 91006593

PARADOXICAL ENHANCEMENT OF INTERLEUKIN-2-MEDIATED CYTOTOXICITY AGAINST K562 CELLS BY ADDITION OF A LOW DOSE OF METHOTREXATE

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CANCER IMMUNOL IMMUNOTHER 32 (1). 1990. 8-12. CODEN: CIIMD

Full Journal Title: Cancer Immunology Immunotherapy

Language: ENGLISH

In vitro effects of methotrexate (MTX) on interleukin-2(IL-2)-mediated cytotoxicity of peripheral blood mononculear cells (PBMC) were studied. PBMC were incubated with human recombinant IL-2 (25 U/ml) for 72 h; during the last 24 h, various concentrations (10 pM-1 1 .mu.M) of MTX were added to the culture. Cytotoxicity against k562 cells was measured by a 4-h 51Cr-release assay. The IL-2-mediated cytotoxicity was paradoxically increased at around a concentration (10 nM) MTX. Such a low concentration of MTX showed no anti-proliferative effect on cell growth. This enhancement

with 10 nM MTX was shown only in an E-rosette+ (E+) population, but not in E-rosette- (E-). In addition, when E+ cells were treated with an anti-CD16 monoclonal antibody plus complement after incubation with IL-2 and MTX, MTX-induced enhancement was lost, suggesting that an E+CD16+ cell population was mainly involved in this augmentation. Positively sorted E+CD16+ cells showed similar enhancement of cytotoxicity after treatment with IL-2 plus MTX. On the other hand, MTX treatment did not show the phenotypical changes including of the E+CD16+ cells, indicating that this treatment did not affect the differentiation and proliferation of the specific cell subset. Our results indicate that a low dose of MTX could have a role in the regulation of immunological anti-cancer surveillance systems through the natural killer and lymphokine-activated cytotoxic cells.

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7729928 BIOSIS Number: 90097928

TROPHOBLAST-DERIVED INTERLEUKIN-6 IL-6 REGULATES HUMAN CHORIONIC GONADOTROPIN RELEASE THROUGH IL-6 RECEPTOR ON HUMAN TROPHOBLASTS

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J CLIN ENDOCRINOL METAB 71 (2). 1990. 436-441. CODEN: JCEMA Full Journal Title: Journal of Clinical Endocrinology & Metabolism Language: ENGLISH

We examined the capacity of trophoblast-derived interleukin-6 (UL-6) to stimulate secretion of placental hormones, including hCG. IL-6 stimulated hCG secretion by trophoblasts to a level similar to that stimulated by a GnRH analog. The analog, however, released hCG by an IL-6-independent mechanism because PM-1, a monoclonal antibody specific for IL-6 receptors (R), failed to block GnRH-mediated responses, but completely blocked IL-6 mediated hCG secretion, suggesting the existence of two distinct regulatory pathways for hCG release. Immunohistochemical analysis with another IL-6-R-specific antibody. MT-18, showed that IL-6-R was located only on the trophoblast layer of the placenta. Our data revealed the existence of a local regulatory network by which trophoblast-derived IL-6 interacts with IL-6-R on the trophoblasts, resulting in hCG release. Thus, two different regulatory networks, an IL-6 and IL-6-R system and a GnRH and GnRH-R system, regulate hCG release by human trophoblasts independently.

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7692329 BIOSIS Number: 90060329

MOLECULAR VARIANTS OF CHOLECYSTOKININ AFTER ENDOGENOUS STIMULATION IN HUMANS A TIME STUDY

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AM J PHYSIOL 258 (6 PART 1). 1990. G951-G957. CODEN: AJPHA Full Journal Title: American Journal of Physiology

X

Language: ENGLISH

The time-dependent release of molecular variants of cholecystokinin (CCK) into the circulation was studied before and 1,2, and 4 h after a test meal in six healthy volunteers. At each time period, 100 ml of blood were drawn in a manner to inhibit CCK degradation. Plasma was formed and CCK concentrated by Sep-Pak C18 cartridge chromatography. Molecular variants of CCK and gastrin were well separated from each other by high-performance liquid chromatography (HPLC). Molecular forms of CCK and gastrin were measured by radioimmunoassay using an antibody that requires the presence of the carboxyl-terminal phenylalanine amide for full recognition, implying that biologically active forms were detected. HPLC elution positions of using a gastrin-specific antibody. forms were determined gastrin Chromatographic separation of CCK from gastrin forms was complete, allowing separate integration of gastrin and CCK forms. Therefore no substraction of gastrin-like immunoreactivity from CCK-like immunoreactivity (CCK-LI) was necessary and CCK-LI could be directly determined. Peaks of CCK-LI were integrated in the column eluates and the plasma concentrations were calculated. Total plasma CCK-LI rose from a value of 2.4 .+-. 0.6 pM before the test meal to 6.4 .+-. 0.8, 6.6 .+-. 0.9, and 5.8 .+-. 1.2 pM $\overline{1}$, 2, and 4 h postprandially. The major molecular forms released into the circulation eluted on HPLC in the position of CCK-58 and CCK-39 (which coelutes with CCK-33). Minor amounts were detected in the position of CCK-8. There was no significant difference in the relative proportions of the molecular forms released at the different time periods. The high proportions of CCK-58 in human plasma indicate that it expresses a major portion of CCK's biological activity.

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7398030 BIOSIS Number: 89049049

DETECTION AND ANTIGENIC CHARACTERIZATION OF ANTINUCLEAR ANTIBODIES IN CONNECTIVE TISSUE DISEASES

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REV MED LIEGE 44 (19). 1989. 577-591. CODEN: RMLIA

Full Journal Title: Revue Medicale de Liege

Language: FRENCH

determine the correlation between the presence of antinuclear (ANA) and connective tissue disease, a prospective clinical study was conducted on 167 patients with one of the following conditions: systemic lupus erythematosus (SLE), induced lupus, rheumatoid arthritis, scleroderma, mixed connective tissue disease, primary Sjogren's syndrome, dermatomyositis, combined SLE and scleroderma, and psoriatic arthritis. ANA patients' serum were detected and titrated by indirect immunofluorescence, and the pattern of immunofluorescence (homogeneous, peripheral, speckled, nucleolar, centromeric or chromosomal) was noted; ANA characterized using the "nDNA C. L. Sci. Medx", "ENA antigen system" "ANA check" kits from Biolab SA. Serum ANA were found to include and antibodies to native DNA (anti-DNA), deoxyribonucleoprotein (anti-DNP), and extractable nuclear antigens (anti-ENA); included in the last group were (anti-Sm), antibodies to ribonucleoprotein anti-Smith antibodies (anti-U1-RNP), and the antibodies to Ro/SS-A, La/SS-B, Scl-70, Jo-1, PM-1, Ku, centromere and nucleolus. Some ANA were found to be specific for certain diseases, e.g. anti-DNA for lupus, anti-Sm for SLE, anti-Scl-70 and anticentromere for scleroderma. Other antibodies, although not specific, were frequently associated with diseases, e.g. anti-RNP with SLE, anti-Ro/SS-A and anti-La/SS-B with Sjogren's syndrome. Detection and characterization of ANA was concluded to be of prognostic value and could be used as a diagnostic tool and an aid in treatment planning.

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6944784 BIOSIS Number: 87005305

EFFECT OF INTERLEUKIN 1 BETA ON TRANSDUCING MECHANISMS IN 235-1 CLONAL PITUITARY CELLS PART II MODULATION OF CALCIUM FLUXES

SCHETTINI G; MEUCCI O; FLORIO T; SCALA G; LANDOLFI E; GRIMALDI M DEP. PHARMACOL., II SCH. MED., VIA PANSINI 5, 80131 NAPOLI, ITALY. BIOCHEM BIOPHYS RES COMMUN 155 (3). 1988. 1097-1104. CODEN: BBRCA Full Journal Title: Biochemical and Biophysical Research Communications Language: ENGLISH

In the present study we investigated the effect of the interleukin 1 beta on intracellular free calcium concentrations in 235-1 cell line both in basal conditions and after stimulation by the calcium channel activator maitotoxin. Interleukin 1 beta (from 0.01 pM to 10 nM) was unable to significantly affect basal cytosolic free calcium levels in conditions. The preincubation of these cells with interleukin 1 beta for 48th modulates maitotoxin stimulation of calcium fluxes without modifying basal intracellular free calcium levels. Low concentrations of interleuking 1 beta (0.01 pM, 1 pM) caused a marked reduction of intracellular free calcium concentrations increase induced by maitotoxin while higher doses of the monokine potentiated maitotoxin stimulation of calcium fluxes. The specificity of interleukin 1 beta effect was tested by means of polyclonal anti-interleukin 1 beta antibody (titer 1:100) which significantly abolished the inhibitory effect of interleukin 1 beta on free cytosolic calcium levels. These results show that a long lasting interaction of interleukin 1 beta with its receptor is able to influence voltage-sensitive calcium channels activation induced by maitotoxin in 235-1 cells.

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6638080 BIOSIS Number: 86104631

ENHANCED HUMAN MONOCYTE CYTOTOXICITY BY PLATELET-ACTIVATING FACTOR

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IMMUNOLOGY 64 (4). 1988. 715-718. CODEN: IMMUA

Full Journal Title: Immunology

Language: ENGLISH

The capacity of platelet-activating factor (PAF) to enhance human monocyte cytoxicity for WEHI 164 cells was examined. Spontaneous monocyte cytotoxicity was 24 .+-. 2% (mean .+-. SEM, n =9). Preincubation of monocytes with 1 pM-1 nM PAF for 18 hr significantly enhanced cytotoxicity in a dose-related manner, whereas less enhancement was observed at PAF concentrations above 1 nM. Maximal PAF-induced cytotoxicity was 68 .+-. 6%, which was similar to that induced by optimal concentrations of tumour necrosis factor (TNF) and interferon-gamma. The specific PAF antagonist kadsurenone inhibited PAF-induced cytotoxicity but not TNF-induced

cytotoxicity. The inactive PAF analogues lysoPAF and enantioPAF did not increase monocyte cytotoxicity. Two observations suggest that TNF mediates PAF-induced cytotoxicity: specific anti-TNF antibodies inhibited PAF induced cytotoxicity toward WEHI 164 cells, and PAF did not enhance cytotoxicity to TNF-resistent cells. PAF represents a distinct class of phospholipid monocyte activators that increase monocyte cytotoxicity by TNF-dependent mechanisms.

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5427916 BIOSIS Number: 82072719

SMALL NUCLEAR RIBONUCLEOPROTEIN ANTIGENS ARE ABSENT FROM 10S TRANSLATION INHIBITORY RIBONUCLEOPROTEIN BUT PRESENT IN CYTOPLASMIC MESSENGER RIBONUCLEOPROTEIN AND POLYSOMES

BOAK A M; KOVACS S A; AGRIS P F; CHAKRABORTY D; SARKAR S DEP. MED. DIV. BIOL. SCI., UIV. MISSOURI, COLUMBIA, MO. 65211. ARCH BIOCHEM BIOPHYS 248 (1). 1986. 89-100. CODEN: ABBIA Full Journal Title: Archives of Biochemistry and Biophysics Language: ENGLISH

A cytoplasmic 10S ribonucleoprotein particle (iRNP), which is isolated from chick embryonic muscle, is a potent inhibitor of mRNA translation in vitro and contains a 4S translation inhibitory RNA species (iRNA). The iRNP particle shows similarity in size to the small nuclear ribonucleoprotein (snRNP) particles. Certain autoimmune disease patients contain antibodies directed against snRNP antigenic determinants. The possibility that iRNP nuclear particles was tested by related to the ${ t small}$ immunoreactivity with monospecific autoimmune antibodies to six antigenic determinants (Sm, RNP, PM-1, SS-A (Ro), SS-B (La), and Scl-70). By Ouchterlony immunodiffusion assays, the cytoplasmic 10S iRNP did not show any immunoreactivity. Also, a more sensitive hemagglutination inhibition assay for detecting Sm and RNP antigens failed to show reactivity with the Thus, the 10S iRNP particles are distinct from the similarly sized snRNP. However, free and polysomal messenger ribonucleoprotein (mRNP) particles and polysomes also isolated from chick embryonic muscle and analyzed by Ouchterlony immunodiffusion and hemagglutination inhibition for the presence of the antigenic determinants showed reactivity to Sm and RNP autoantibodies, but were not antigenic for the other four antibodies. Some of the Sm antigenic peptides of mRNP particles and polysomes were identical those purified from calf thynus nuclear extract, as judged by Western blot analysis. The association of Sm with free and polysomal mRNP and polysomes suggests that Sm may be involved in some cytoplamic aspects of mRNA metabolism, in addition to a nuclear function in mRNA processing.

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4853405 BIOSIS Number: 79095720

IMMUNOGENETIC STUDIES OF JUVENILE DERMATOMYOSITIS 3. STUDY OF ANTIBODY TO ORGAN-SPECIFIC AND NUCLEAR ANTIGENS

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ARTHRITIS RHEUM 28 (2). 1985. 151-157. CODEN: ARHEA

Full Journal Title: Arthritis and Rheumatism

Language: ENGLISH

Children (90) with definite juvenile dermatomyositis (JDMS), who had been typed, were tested for the presence of tissue or organ-specific antibodies. Sixty had active disease at the time of study. The mean disease duration was 4 yr and 30 had soft tissue calcifications. The following autoantibodies were sought: thyroid, gastric parietal cells, smooth muscle, striated muscle, microsomes, mitochondria, DNA, extractable nuclear antigen, Sm, PM-1, antinuclear antibody (ANA) and rheumatoid factor. Only the ANA and PM-1 were more frequent in patients than in controls (P <0.0002 and P < 0.001, respectively). Higher levels of immune complexes (P < 0.01) were in sera from patients with JDMS than in sera from controls and were correlated with the presence of ANA in patients (P < 0.01). Soft tissue calcification was not associated with any autoantibody or HLA antigen, but with disease duration and activity (P < 0.001 and P < 0.05, respectively). There was no association between the occurrence of any autoantibody and the presence of HLA-B8 or DR3 among the white patients with JDMS. The frequency of autoantibodies in 43 full siblings of children JDMS was not increased. Children with JDMS, with or without HLA-B8/DR3, do not show evidence of a generalized nonspecific antibody response to tissue antigens. The significance of the increased antibody to nuclear antigens ANA and PM-1 remains to be determined.

23/7/23

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4836297 BIOSIS Number: 79078612

HIGH-AFFINITY MONOCLONAL ANTIBODIES FOR AFLATOXINS AND THEIR APPLICATION TO SOLID-PHASE IMMUNOASSAYS

GROOPMAN J D; TRUDEL L J; DONAHUE P R; MARSHAK-ROTHSTEIN A; WOGAN G N BOSTON UNIVERSITY SCHOOL PUBLIC HEALTH, HUBERT H. HUMPHREY CANCER RESEARCH CENTER, DEPARTMENT MICROBIOLOGY, SCHOOL MEDICINE, 80 EAST CONCORD STREET, BOSTON, MASS. 02118.

PROC NATL ACAD SCI U S A 81 (24). 1984 (RECD. 1985). 7728-7731.

CODEN: PNASA

Full Journal Title: Proceedings of the National Academy of Sciences of the United States of America

Language: ENGLISH

Monoclonal antibodies specific for aflatoxin B1, aflatoxin B2, aflatoxin and the major aflatoxin-DNA adducts were obtained following fusion of M1 mouse SP-2 myeloma cells with spleen cells of mice immunized with aflatoxin covalently bound to bovine gamma globulin. The aflatoxin-modified protein used to immunize mice was produced chemically by activating aflatoxin B1 to a 2,3-epoxide derivative, which then covalently bound to the protein. One of the monoclonal antibodies isolated (2B11) was a high-affinity IgM antibody with an affinity constant for aflatoxin B1, aflatoxin B2 and aflatoxin M1 of .apprx. 1 .times. 109 l/mol. In a competitive radioimmunoassay using [3H]aflatoxin B1, 3 pmol (1 ng) of aflatoxin B1, aflatoxin B2 or aflatoxin M1 caused 50% inhibition with this antibody. The antibody also had significant cross-reactivity for the major aflatoxin-DNA adducts: 2,3-dihydro-2-(N7-guanyl)-3-hydroxyaflatoxin B1 and 2,3-dihydro-2-(N5-formyl-2',5',6'-triamino-4' oxo-N5-pyrimidyl)-3-hydroxyaf latoxin B1. The antibody was also covalently bound to Sepharose-4B and used in a column-based solid-phase immunosorbent assay system. Aflatoxins added in vitro to phosphate buffer, human urine, human serum or human milk at levels expected to be obtained in human samples acquired from environmentally exposed individuals were quantitatively recovered by applying the mixture to this antibody affinity column purification system. Preliminary studies using urine samples from rats injected with radiolabeled aflatoxin B1 have also indicated that aflatoxin metabolites can be isolated by these methods. The monoclonal antibody affinity columns can be regenerated for multiple use. Therefore, the monoclonal antibodies and their application to affinity chromatography represents a useful and rapid technique to purify environmentally occurring levels of this carcinogen and some of its metabolites for quantitative measurements.

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Set	Items	Description
S1	622	IL6
S2	301812	RECEPTOR?
S3	12338	INTERLEUKIN(W)6
S4	12505	S1 OR S3
S5	2087	S4 AND S2
S6	259799	ANTIBOD?
S7	463	S5 AND S6
S8	173	IL(W)6R
S9	64	S6 AND S8
S10	281	<pre>INTERLEUKIN(W)6(W)RECEPTOR?</pre>
S11	63	S6 AND S10
S12	99	S9 OR S11
S13	1717319	PY=(1993:1996)
S14	25	S12 NOT S13
S15	483053	NEUTRALI? OR INHIBIT?
S16	12	S14 AND S15
S17	30	<pre>HUMAN(W) IL(W) 6(W) RECEPTOR?</pre>
S18	13	S6 AND S17
S19	9024	CHIMERIC OR HUMANIZ? OR RESHAP?
S20	1	S18 AND S19
S21	2	S10 AND S6 AND S19
S22	278	PM(W)1
S23	24	S6 AND S22
?		